

# SEQUENCE LISTING

<110> Bristol-Myers Squibb Company

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<150> 60/263,678

<151> 2001-01-23

<150> 60/273,037

<151> 2001-03-02

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<170> PatentIn version 3.0

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atgcagagtc cctgagccca cctcccagcc ctctcctcat tctctgaacc cactgtggtg 3333  
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gtttaaaaca gcctaacaaa gacacttgcc tgtgg 3428

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<212> PRT  
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Ala Cys Ala Trp Gly His Thr Lys Pro Leu Asp Leu Gly Gly Gln Asp  
20 25 30

Val Arg Asn Cys Ser Thr Asn Pro Pro Tyr Leu Pro Val Thr Val Val  
35 40 45

Asn Thr Thr Met Ser Leu Thr Ala Leu Arg Gln Gln Met Gln Thr Gln  
50 55 60

Asn Leu Ser Ala Tyr Ile Ile Pro Gly Thr Asp Ala His Met Asn Glu  
65 70 75 80



Tyr Ile Gly Gln His Asp Glu Arg Arg Ala Trp Ile Thr Gly Phe Thr  
85 90 95

Gly Ser Ala Gly Thr Ala Val Val Thr Met Lys Lys Ala Ala Val Trp  
100 105 110

Thr Asp Ser Arg Tyr Trp Thr Gln Ala Glu Arg Gln Met Asp Cys Asn  
115 120 125

Trp Glu Leu His Lys Glu Val Gly Thr Thr Pro Ile Val Thr Trp Leu  
130 135 140

Leu Thr Glu Ile Pro Ala Gly Gly Arg Val Gly Phe Asp Pro Phe Leu  
145 150 155 160

Leu Ser Ile Asp Thr Trp Glu Ser Tyr Asp Leu Ala Leu Gln Gly Ser  
165 170 175

Asn Arg Gln Leu Val Ser Ile Thr Thr Asn Leu Val Asp Leu Val Trp  
180 185 190

Gly Ser Glu Arg Pro Pro Val Pro Asn Gln Pro Ile Tyr Ala Leu Gln  
195 200 205

Glu Ala Phe Thr Gly Ser Thr Trp Gln Glu Lys Val Ser Gly Val Arg  
210 215 220

Ser Gln Met Gln Lys His Gln Lys Val Pro Thr Ala Val Leu Leu Ser  
225 230 235 240

Ala Leu Glu Glu Thr Ala Trp Leu Phe Asn Leu Arg Ala Ser Asp Ile  
245 250 255

Pro Tyr Asn Pro Phe Phe Tyr Ser Tyr Thr Leu Leu Thr Asp Ser Ser  
260 265 270

Ile Arg Leu Phe Ala Asn Lys Ser Arg Phe Ser Ser Glu Thr Leu Ser  
275 280 285

Tyr Leu Asn Ser Ser Cys Thr Gly Pro Met Cys Val Gln Ile Glu Asp  
290 295 300

Tyr Ser Gln Val Arg Asp Ser Ile Gln Ala Tyr Ser Leu Gly Asp Val  
305 310 315 320

Arg Ile Trp Ile Gly Thr Ser Tyr Thr Met Tyr Gly Ile Tyr Glu Met  
325 330 335

Ile Pro Arg Glu Lys Leu Val Thr Asp Thr Tyr Ser Pro Val Met Met  
340 345 350

Thr Lys Ala Val Lys Asn Ser Lys Glu Gln Ala Leu Leu Lys Ala Ser  
355 360 365

His Val Arg Asp Ala Val Ala Val Ile Arg Tyr Leu Val Trp Leu Glu  
370 375 380

Lys Asn Val Pro Lys Gly Thr Val Asp Glu Phe Ser Gly Ala Glu Ile  
385 390 395 400

Val Asp Lys Phe Arg Gly Glu Glu Gln Phe Ser Ser Gly Pro Ser Phe  
405 410 415

Glu Thr Ile Ser Ala Ser Gly Leu Asn Ala Ala Leu Ala His Tyr Ser  
420 425 430

Pro Thr Lys Glu Leu Asn Arg Lys Leu Ser Ser Asp Glu Met Tyr Leu  
435 440 445

Leu Asp Ser Gly Gly Gln Tyr Trp Asp Gly Thr Thr Asp Ile Thr Arg  
450 455 460

Thr Val His Trp Gly Thr Pro Ser Ala Phe Gln Lys Glu Ala Tyr Thr  
465 470 475 480

Arg Val Leu Ile Gly Asn Ile Asp Leu Ser Arg Leu Ile Phe Pro Ala  
485 490 495

Ala Thr Ser Gly Arg Met Val Glu Ala Phe Ala Arg Arg Ala Leu Trp  
500 505 510

Asp Ala Gly Leu Asn Tyr Gly His Gly Thr Gly His Gly Ile Gly Asn  
515 520 525

Phe Leu Cys Val His Glu Trp Pro Val Gly Phe Gln Ser Asn Asn Ile

530

535

540

Ala Met Ala Lys Gly Met Phe Thr Ser Ile Glu Pro Gly Tyr Tyr Lys  
545 550 555 560

Asp Gly Glu Phe Gly Ile Arg Leu Glu Asp Val Ala Leu Val Val Glu  
565 570 575

Ala Lys Thr Lys Tyr Pro Gly Glu Leu Pro Asp Leu Val Val Ser Phe  
580 585 590

Val Pro Tyr Asp Arg Asn Leu Ile Asp Val Ser Leu Leu Ser Pro Glu  
595 600 605

His Leu Gln Tyr Leu Asn Arg Tyr Tyr Gln Thr Ile Arg Glu Lys Val  
610 615 620

Gly Pro Glu Leu Gln Arg Arg Gln Leu Leu Glu Glu Phe Glu Trp Leu  
625 630 635 640

Gln Gln His Thr Glu Pro Leu Ala Ala Arg Ala Pro Asp Thr Ala Ser  
645 650 655

Trp Ala Ser Val Leu Val Val Ser Thr Leu Ala Ile Leu Gly Trp Ser  
660 665 670

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<220>  
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<222> (7)..(1065)

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Met Ala Ser Ser Trp Pro Pro Leu Glu Leu Gln Ser Ser Asn  
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cag agc cag ctc ttc cct caa aat gct acg gcc tgt gac aat gct cca 96  
Gln Ser Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro  
15 20 25 30

gaa gcc tgg gac ctg ctg cac aga gtg ctg ccg aca ttt atc atc tcc	144
Glu Ala Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser	
35 40 45	
atc tgt ttc ttc ggc ctc cta ggg aac ctt ttt gtc ctg ttg gtc ttc	192
Ile Cys Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe	
50 55 60	
ctc ctg ccc cgg cgg caa ctg aac gtg gca gaa atc tac ctg gcc aac	240
Leu Leu Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn	
65 70 75	
ctg gca gcc tct gat ctg gtg ttt gtc ttg ggc ttg ccc ttc tgg gca	288
Leu Ala Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala	
80 85 90	
gag aat atc tgg aac cag ttt aac tgg cct ttc gga gcc ctc ctc tgc	336
Glu Asn Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys	
95 100 105 110	
cgt gtc atc aac ggg gtc atc aag gcc aat ttg ttc atc agc atc ttc	384
Arg Val Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe	
115 120 125	
ctg gtg gtg gcc atc agc cag gac cgc tac cgc gtg ctg gtg cac cct	432
Leu Val Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro	
130 135 140	
atg gcc agc gga agg cag cag cgg cgg agg cag gcc cgg gtc acc tgc	480
Met Ala Ser Gly Arg Gln Gln Arg Arg Arg Gln Ala Arg Val Thr Cys	
145 150 155	
gtg ctc atc tgg gtt gtg ggg ggc ctc ttg agc atc ccc aca ttc ctg	528
Val Leu Ile Trp Val Val Gly Leu Leu Ser Ile Pro Thr Phe Leu	
160 165 170	
ctg cga tcc atc caa gcc gtc cca gat ctg aac atc acc gcc tgc atc	576
Leu Arg Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile	
175 180 185 190	
ctg ctc ctc ccc cat gag gcc tgg cac ttt gca agg att gtg gag tta	624
Leu Leu Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu	
195 200 205	
aat att ctg ggt ttc ctc cta cca ctg gct gcg atc gtc ttc ttc aac	672
Asn Ile Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn	
210 215 220	
tac cac atc ctg gcc tcc ctg cga acg cgg gag gag gtc agc agg aca	720
Tyr His Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr	
225 230 235	
aga gtg cgg ggg ccg aag gat agc aag acc aca gcg ctg atc ctc acg	768
Arg Val Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr	
240 245 250	
ctc gtg gtt gcc ttc ctg gtc tgc tgg gcc cct tac cac ttc ttt gcc	816

Leu Val Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala	
255 260 265 270	
ttc ctg gaa ttc tta ttc cag gtg caa gca gtc cga ggc tgc ttt tgg	864
Phe Leu Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp	
275 280 285	
gag gac ttc att gac ctg ggc ctg caa ttg gcc aac ttc ttt gcc ttc	912
Glu Asp Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe	
290 295 300	
act aac agc tcc ctg aat cca gta att tat gtc ttt gtg ggc cgg ctc	960
Thr Asn Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu	
305 310 315	
ttc agg acc aag gtc tgg gaa ctt tat aaa caa tgc acc cct aaa agt	1008
Phe Arg Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser	
320 325 330	
ctt gct cca ata tct tca tcc cat agg aaa gaa atc ttc caa ctt ttc	1056
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Trp Arg Asn	

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Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser Ile Cys	
35 40 45	
Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe Leu Leu	
50 55 60	
Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala	
65 70 75 80	
Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn	
85 90 95	

Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val  
 100 105 110

Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val  
 115 120 125

Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala  
 130 135 140

Ser Gly Arg Gln Gln Arg Arg Arg Gln Ala Arg Val Thr Cys Val Leu  
 145 150 155 160

Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg  
 165 170 175

Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu  
 180 185 190

Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile  
 195 200 205

Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His  
 210 215 220

Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val  
 225 230 235 240

Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val  
 245 250 255

Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu  
 260 265 270

Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp  
 275 280 285

Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn  
 290 295 300

Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg  
 305 310 315 320

Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala  
 325 330 335

Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg  
 340 345 350

Asn

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<220>  
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cag agc cag ctc ttc cct caa aat gct acg gcc tgt gac aat gct cca 96  
 Gln Ser Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro  
 15 20 25 30

gaa gcc tgg gac ctg ctg cac aga gtg ctg ccg aca ttt atc atc tcc 144  
 Glu Ala Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser  
 35 40 45

atc tgt ttc ttc ggc ctc cta ggg aac ctt ttt gtc ctg ttg gtc ttc 192  
 Ile Cys Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe  
 50 55 60

ctc ctg ccc cgg cgg caa ctg aac gtg gca gaa atc tac ctg gcc aac 240  
 Leu Leu Pro Arg Arg Gln Leu Val Ala Glu Ile Tyr Leu Ala Asn  
 65 70 75

ctg gca gcc tct gat ctg gtg ttt gtc ttg ggc ttg ccc ttc tgg gca 288  
 Leu Ala Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala  
 80 85 90

gag aat atc tgg aac cag ttt aac tgg cct ttc gga gcc ctc ctc tgc 336  
 Glu Asn Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys  
 95 100 105 110

cgt gtc atc aac ggg gtc atc aag gcc aat ttg ttc atc agc atc ttc 384  
 Arg Val Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe  
 115 120 125

ctg gtg gtg gcc atc agc cag gac cgc tac cgc gtg ctg gtg cac cct 432  
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130	135	140	
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gtg ctc atc tgg gtt gtg ggg ggc ctc ttg agc atc ccc aca ttc ctg Val Leu Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu 160 165 170			528
ctg cga tcc atc caa gcc gtc cca gat ctg aac atc acc gcc tgc atc Leu Arg Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile 175 180 185 190			576
ctg ctc ctc ccc cat gag gcc tgg cac ttt gca agg att gtg gag tta Leu Leu Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu 195 200 205			624
aat att ctg ggt ttc ctc cta cca ctg gct gcg atc gtc ttc ttc aac Asn Ile Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn 210 215 220			672
tac cac atc ctg gcc tcc ctg cga acg cgg gag gag gtc agc agg aca Tyr His Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr 225 230 235			720
aga gtg cgg ggg ccg aag gat agc aag acc aca gcg ctg atc ctc acg Arg Val Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr 240 245 250			768
ctc gtg gtt gcc ttc ctg gtc tgc tgg gcc cct tac cac ttc ttt gcc Leu Val Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala 255 260 265 270			816
ttc ctg gaa ttc tta ttc cag gtg caa gca gtc cga ggc tgc ttt tgg Phe Leu Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp 275 280 285			864
gag gac ttc att gac ctg ggc ctg caa ttg gcc aac ttc ttt gcc ttc Glu Asp Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe 290 295 300			912
act aac agc tcc ctg aat cca gtaatt tat gtc ttt gtg ggc cag ctc Thr Asn Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Gln Leu 305 310 315			960
ttc agg acc aag gtc tgg gaa ctt tat aaa caa tgc acc cct aaa agt Phe Arg Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser 320 325 330			1008
ctt gct cca ata tct tca tcc cat agg aaa gaa atc ttc caa ctt ttc Leu Ala Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe 335 340 345 350			1056
tggtg cgg aat taaaacagca ttgaacc Trp Arg Asn			1082



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 <213> homo sapiens

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Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro Glu Ala  
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Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser Ile Cys  
 35 40 45

Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe Leu Leu  
 50 55 60

Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala  
 65 70 75 80

Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn  
 85 90 95

Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val  
 100 105 110

Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val  
 115 120 125

Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala  
 130 135 140

Ser Gly Arg Gln Gln Arg Arg Arg Gln Ala Arg Val Thr Cys Val Leu  
 145 150 155 160

Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg  
 165 170 175

Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu  
 180 185 190

Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile  
 195 200 205

Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His  
 210 215 220

Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val  
 225 230 235 240

Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val  
 245 250 255

Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu  
 260 265 270

Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp  
 275 280 285

Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn  
 290 295 300

Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Gln Leu Phe Arg  
 305 310 315 320

Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala  
 325 330 335

Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg  
 340 345 350

Asn

<210> 9  
 <211> 1082  
 <212> DNA  
 <213> homo sapiens

<220>  
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 <222> (7)..(1065)

<400> 9

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48

cag agc cag ctc ttc cct caa aat gct acg gcc tgt gac aat gct cca Gln Ser Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro 15 20 25 30	96
gaa gcc tgg gac ctg ctg cac aga gtg ctg cca aca ttt atc atc tcc Glu Ala Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser 35 40 45	144
atc tgt ttc ttc ggc ctc cta ggg aac ctt ttt gtc ctg ttg gtc ttc Ile Cys Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe 50 55 60	192
ctc ctg ccc cgg cgg caa ctg aac gtg gca gaa atc tac ctg gcc aac Leu Leu Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn 65 70 75	240
ctg gca gcc tct gat ctg gtg ttt gtc ttg ggc ttg ccc ttc tgg gca Leu Ala Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala 80 85 90	288
gag aat atc tgg aac cag ttt aac tgg cct ttc gga gcc ctc ctc tgc Glu Asn Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys 95 100 105 110	336
cgt gtc atc aac ggg gtc atc aag gcc aat ttg ttc atc agc atc ttc Arg Val Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe 115 120 125	384
ctg gtg gtg gcc atc agc cag gac cgc tac cgc gtg ctg gtg cac cct Leu Val Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro 130 135 140	432
atg gcc agc gga agg cag cag cgg cgg agg cag gcc cgg gtc acc tgc Met Ala Ser Gly Arg Gln Gln Arg Arg Arg Gln Ala Arg Val Thr Cys 145 150 155	480
gtg ctc atc tgg gtt gtg ggg ggc ctc ttg agc atc ccc aca ttc ctg Val Leu Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu 160 165 170	528
ctg cga tcc atc caa gcc gtc cca gat ctg aac atc acc gcc tgc atc Leu Arg Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile 175 180 185 190	576
ctg ctc ctc ccc cat gag gcc tgg cac ttt gca agg att gtg gag tta Leu Leu Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu 195 200 205	624
aat att ctg ggt ttc ctc cta cca ctg gct gcg atc gtc ttc ttc aac Asn Ile Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn 210 215 220	672
tac cac atc ctg gcc tcc ctg cga acg cgg gag gag gtc agc agg aca Tyr His Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr 225 230 235	720

aga gtg cgg ggg ccg aag gat agc aag acc aca gcg ctg atc ctc acg 768  
 Arg Val Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr  
 240 245 250

ctc gtg gtt gcc ttc ctg gtc tgc tgg gcc cct tac cac ttc ttt gcc 816  
 Leu Val Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala  
 255 260 265 270

ttc ctg gaa ttc tta ttc cag gtg caa gca gtc cga ggc tgc ttt tgg 864  
 Phe Leu Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp  
 275 280 285

gag gac ttc att gac ctg ggc ctg caa ttg gcc aac ttc ttt gcc ttc 912  
 Glu Asp Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe  
 290 295 300

act aac agc tcc ctg aat cca gta att tat gtc ttt gtg ggc cgg ctc 960  
 Thr Asn Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu  
 305 310 315

ttc agg acc aag gtc tgg gaa ctt tat aaa caa tgc acc cct aaa agt 1008  
 Phe Arg Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser  
 320 325 330

ctt gct cca ata tct tca tcc cat agg aaa gaa atc ttc caa ctt ttc 1056  
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 335 340 345 350

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 Trp Arg Asn

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Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser Ile Cys  
 35 40 45

Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe Leu Leu  
 50 55 60

Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala

65

70

75

80

Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn  
85 90 95

Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val  
100 105 110

Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val  
115 120 125

Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala  
130 135 140

Ser Gly Arg Gln Gln Arg Arg Arg Gln Ala Arg Val Thr Cys Val Leu  
145 150 155 160

Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg  
165 170 175

Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu  
180 185 190

Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile  
195 200 205

Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His  
210 215 220

Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val  
225 230 235 240

Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val  
245 250 255

Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu  
260 265 270

Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp  
275 280 285

Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn  
290 295 300

Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg  
305 310 315 320

Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala  
325 330 335

Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg  
340 345 350

Asn

<210> 11  
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<212> DNA  
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<220>  
<221> CDS  
<222> (1)..(1173)

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Met Phe Ser Pro Trp Lys Ile Ser Met Phe Leu Ser Val Arg Glu Asp  
1 5 10 15  
tcc gtg ccc acc acg gcc tct ttc agc gcc gac atg ctc aat gtc acc 96  
Ser Val Pro Thr Thr Ala Ser Phe Ser Ala Asp Met Leu Asn Val Thr  
20 25 30  
ttg caa ggg ccc act ctt aac ggg acc ttt gcc cag agc aaa tgc ccc 144  
Leu Gln Gly Pro Thr Leu Asn Gly Thr Phe Ala Gln Ser Lys Cys Pro  
35 40 45  
caa gtg gag tgg ctg ggc tgg ctc aac acc atc cag ccc ccc ttc ctc 192  
Gln Val Glu Trp Leu Gly Trp Leu Asn Thr Ile Gln Pro Pro Phe Leu  
50 55 60  
tgg gtg ctg ttc gtg ctg gcc acc cta gag aac atc ttt gtc ctc agc 240  
Trp Val Leu Phe Val Leu Ala Thr Leu Glu Asn Ile Phe Val Leu Ser  
65 70 75 80  
gtc ttc tgc ctg cac aag agc agc tgc acg gtg gca gag atc tac ctg 288  
Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu  
85 90 95  
ggg aac ctg gcc gca gca gac ctg atc ctg gcc tgc ggg ctg ccc ttc 336  
Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe  
100 105 110  
tgg gcc atc acc atc tcc aac aac ttc gac tgg ctc ttt ggg gag acg 384

Trp	Ala	Ile	Thr	Ile	Ser	Asn	Asn	Phe	Asp	Trp	Leu	Phe	Gly	Glu	Thr		
		115					120					125					
ctc	tgc	cgc	gtg	gtg	aat	gcc	att	atc	tcc	atg	aac	ctg	tac	agc	agc		432
Leu	Cys	Arg	Val	Val	Asn	Ala	Ile	Ile	Ser	Met	Asn	Leu	Tyr	Ser	Ser		
		130				135					140						
atc	tgt	ttc	ctg	atg	ctg	gtg	agc	atc	gac	cgc	tac	ctg	gcc	ctg	gtg		480
Ile	Cys	Phe	Leu	Met	Leu	Val	Ser	Ile	Asp	Arg	Tyr	Leu	Ala	Leu	Val		
					150					155					160		
aaa	acc	atg	tcc	atg	ggc	cgg	atg	cgc	ggc	gtg	cgc	tgg	gcc	aag	ctc		528
Lys	Thr	Met	Ser	Met	Gly	Arg	Met	Arg	Gly	Val	Arg	Trp	Ala	Lys	Leu		
				165					170					175			
tac	agc	ttg	gtg	atc	tgg	ggg	tgt	acg	ctg	ctc	ctg	agc	tca	ccc	atg		576
Tyr	Ser	Leu	Val	Ile	Trp	Gly	Cys	Thr	Leu	Leu	Leu	Ser	Ser	Pro	Met		
			180					185					190				
ctg	gtg	ttc	cgg	acc	atg	aag	gag	tac	agc	gat	gag	ggc	cac	aac	gtc		624
Leu	Val	Phe	Arg	Thr	Met	Lys	Glu	Tyr	Ser	Asp	Glu	Gly	His	Asn	Val		
		195					200					205					
acc	gct	tgt	gtc	atc	agc	tac	cca	tcc	ctc	atc	tgg	gaa	gtg	ttc	acc		672
Thr	Ala	Cys	Val	Ile	Ser	Tyr	Pro	Ser	Leu	Ile	Trp	Glu	Val	Phe	Thr		
		210				215					220						
aac	atg	ctc	ctg	aat	gtc	gtg	ggc	ttc	ctg	ctg	ccc	ctg	agt	gtc	atc		720
Asn	Met	Leu	Leu	Asn	Val	Val	Gly	Phe	Leu	Leu	Pro	Leu	Ser	Val	Ile		
					230					235					240		
acc	ttc	tgc	acg	atg	cag	atc	atg	cag	gtg	ctg	cgg	aac	aac	gag	atg		768
Thr	Phe	Cys	Thr	Met	Gln	Ile	Met	Gln	Val	Leu	Arg	Asn	Asn	Glu	Met		
				245				250						255			
cag	aag	ttc	aag	gag	atc	cag	acg	gag	agg	agg	gcc	acg	gtg	cta	gtc		816
Gln	Lys	Phe	Lys	Glu	Ile	Gln	Thr	Glu	Arg	Arg	Ala	Thr	Val	Leu	Val		
			260					265					270				
ctg	gtt	gtg	ctg	ctg	cta	ttc	atc	atc	tgc	tgg	ctg	ccc	ttc	cag	atc		864
Leu	Val	Val	Leu	Leu	Leu	Phe	Ile	Ile	Cys	Trp	Leu	Pro	Phe	Gln	Ile		
			275				280					285					
agc	acc	ttc	ctg	gat	acg	ctg	cat	cgc	ctc	ggc	atc	ctc	tcc	agc	tgc		912
Ser	Thr	Phe	Leu	Asp	Thr	Leu	His	Arg	Leu	Gly	Ile	Leu	Ser	Ser	Cys		
		290				295					300						
cag	gac	gag	cgc	atc	atc	gat	gta	atc	aca	cag	atc	gcc	tcc	ttc	atg		960
Gln	Asp	Glu	Arg	Ile	Ile	Asp	Val	Ile	Thr	Gln	Ile	Ala	Ser	Phe	Met		
		305			310					315					320		
gcc	tac	agc	aac	agc	tgc	ctc	aac	cca	ctg	gtg	tac	gtg	atc	gtg	ggc		1008
Ala	Tyr	Ser	Asn	Ser	Cys	Leu	Asn	Pro	Leu	Val	Tyr	Val	Ile	Val	Gly		
				325					330					335			
aag	cgc	ttc	cga	aag	aag	tct	tgg	gag	gtg	tac	cag	gga	gtg	tgc	cag		1056
Lys	Arg	Phe	Arg	Lys	Lys	Ser	Trp	Glu	Val	Tyr	Gln	Gly	Val	Cys	Gln		

340	345	350	
aaa ggg ggc tgc agg tca gaa ccc att cag atg gag aac tcc atg ggc			1104
Lys Gly Gly Cys Arg Ser Glu Pro Ile Gln Met Glu Asn Ser Met Gly			
355	360	365	
aca ctg cgg acc tcc atc tcc gtg gaa cgc cag att cac aaa ctg cag			1152
Thr Leu Arg Thr Ser Ile Ser Val Glu Arg Gln Ile His Lys Leu Gln			
370	375	380	
gac tgg gca ggg agc aga cag tgagcaaacg ccagcagggc tgctgtgaat			1203
Asp Trp Ala Gly Ser Arg Gln			
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cccgtgtgtt ctccgtccct gcccagcaa gacaacttag atctccagga gaactgccat			1563
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gcactgtagg caagacccaa gaaagagaag gagccatctc catcttgaag gaactcaaag			1863
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ataactattg cacaaccacc tgtccctgcc tcagttccct tttatgtaac atgaagtcgt			2043
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gtgctgagac cccccaccac cagccggtac ctgggaaggg ggagagtgca ggctgtctca			2463
gggactgttc ctgtctcagc aaccaaggga ttgttctctgt caatcaatgg tttattggaa			2523



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 cgggagaaga gcggccctat gcatggtgta gatgccctga taaagaacat ctgtcctgtg 3603  
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 aaaaaaaaaa 3733

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 <213> homo sapiens

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Ser Val Pro Thr Thr Ala Ser Phe Ser Ala Asp Met Leu Asn Val Thr  
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Leu Gln Gly Pro Thr Leu Asn Gly Thr Phe Ala Gln Ser Lys Cys Pro  
 35 40 45

Gln Val Glu Trp Leu Gly Trp Leu Asn Thr Ile Gln Pro Pro Phe Leu  
 50 55 60

Trp Val Leu Phe Val Leu Ala Thr Leu Glu Asn Ile Phe Val Leu Ser  
 65 70 75 80

Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu  
 85 90 95

Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe  
 100 105 110

Trp Ala Ile Thr Ile Ser Asn Asn Phe Asp Trp Leu Phe Gly Glu Thr  
 115 120 125

Leu Cys Arg Val Val Asn Ala Ile Ile Ser Met Asn Leu Tyr Ser Ser  
 130 135 140

Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg Tyr Leu Ala Leu Val  
 145 150 155 160

Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys Leu  
 165 170 175

Tyr Ser Leu Val Ile Trp Gly Cys Thr Leu Leu Leu Ser Ser Pro Met  
 180 185 190

Leu Val Phe Arg Thr Met Lys Glu Tyr Ser Asp Glu Gly His Asn Val  
 195 200 205

Thr Ala Cys Val Ile Ser Tyr Pro Ser Leu Ile Trp Glu Val Phe Thr  
 210 215 220

Asn Met Leu Leu Asn Val Val Gly Phe Leu Leu Pro Leu Ser Val Ile  
 225 230 235 240

Thr Phe Cys Thr Met Gln Ile Met Gln Val Leu Arg Asn Asn Glu Met  
 245 250 255

Gln Lys Phe Lys Glu Ile Gln Thr Glu Arg Arg Ala Thr Val Leu Val  
 260 265 270

Leu Val Val Leu Leu Leu Phe Ile Ile Cys Trp Leu Pro Phe Gln Ile  
 275 280 285

Ser Thr Phe Leu Asp Thr Leu His Arg Leu Gly Ile Leu Ser Ser Cys  
 290 295 300

Gln Asp Glu Arg Ile Ile Asp Val Ile Thr Gln Ile Ala Ser Phe Met  
 305 310 315 320

Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val Tyr Val Ile Val Gly  
 325 330 335

Lys Arg Phe Arg Lys Lys Ser Trp Glu Val Tyr Gln Gly Val Cys Gln  
 340 345 350

Lys Gly Gly Cys Arg Ser Glu Pro Ile Gln Met Glu Asn Ser Met Gly  
 355 360 365

Thr Leu Arg Thr Ser Ile Ser Val Glu Arg Gln Ile His Lys Leu Gln  
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Asp Trp Ala Gly Ser Arg Gln  
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 agaaggaccc tgagccccag gcgccagcca caggactctg ctgcagaggg gggttgtgta 180  
 cagatagtag gctttacgcc tagcttcgaa atg gat aac gtc ctc ccg gtg gac 234  
 Met Asp Asn Val Leu Pro Val Asp  
 1 5

tca gac ctc tcc cca aac atc tcc act aac acc tcg gaa ccc aat cag	282
Ser Asp Leu Ser Pro Asn Ile Ser Thr Asn Thr Ser Glu Pro Asn Gln	
10 15 20	
ttc gtg caa cca gcc tgg caa att gtc ctt tgg gca gct gcc tac acg	330
Phe Val Gln Pro Ala Trp Gln Ile Val Leu Trp Ala Ala Ala Tyr Thr	
25 30 35 40	
gtc att gtg gtg acc tct gtg gtg ggc aac gtg gta gtg atg tgg atc	378
Val Ile Val Val Thr Ser Val Val Gly Asn Val Val Val Met Trp Ile	
45 50 55	
atc tta gcc cac aaa aga atg agg aca gtg acg aac tat ttt ctg gtg	426
Ile Leu Ala His Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Leu Val	
60 65 70	
aac ctg gcc ttc gcg gag gcc tcc atg gct gca ttc aat aca gtg gtg	474
Asn Leu Ala Phe Ala Glu Ala Ser Met Ala Ala Phe Asn Thr Val Val	
75 80 85	
aac ttc acc tat gct gtc cac aac gaa tgg tac tac ggc ctg ttc tac	522
Asn Phe Thr Tyr Ala Val His Asn Glu Trp Tyr Tyr Gly Leu Phe Tyr	
90 95 100	
tgc aag ttc cac aac ttc ttt ccc atc gcc gct gtc ttc gcc agt atc	570
Cys Lys Phe His Asn Phe Phe Pro Ile Ala Val Phe Ala Ser Ile	
105 110 115 120	
tac tcc atg acg gct gtg gcc ttt gat agg tac atg gcc atc ata cat	618
Tyr Ser Met Thr Ala Val Ala Phe Asp Arg Tyr Met Ala Ile Ile His	
125 130 135	
ccc ctc cag ccc cgg ctg tca gcc aca gcc acc aaa gtg gtc atc tgt	666
Pro Leu Gln Pro Arg Leu Ser Ala Thr Ala Thr Lys Val Val Ile Cys	
140 145 150	
gtc atc tgg gtc ctg gct ctc ctg ctg gcc ttc ccc cag ggc tac tac	714
Val Ile Trp Val Leu Ala Leu Leu Leu Ala Phe Pro Gln Gly Tyr Tyr	
155 160 165	
tca acc aca gag acc atg ccc agc aga gtc gtg tgc atg atc gaa tgg	762
Ser Thr Thr Glu Thr Met Pro Ser Arg Val Val Cys Met Ile Glu Trp	
170 175 180	
cca gag cat ccg aac aag att tat gag aaa gtg tac cac atc tgt gtg	810
Pro Glu His Pro Asn Lys Ile Tyr Glu Lys Val Tyr His Ile Cys Val	
185 190 195 200	
act gtg ctg atc tac ttc ctc ccc ctg ctg gtg att ggc tat gca tac	858
Thr Val Leu Ile Tyr Phe Leu Pro Leu Leu Val Ile Gly Tyr Ala Tyr	
205 210 215	
acc gta gtg gga atc aca cta tgg gcc agt gag atc ccc ggg gac tcc	906
Thr Val Val Gly Ile Thr Leu Trp Ala Ser Glu Ile Pro Gly Asp Ser	
220 225 230	
tct gac cgc tac cac gag caa gtc tct gcc aag cgc aag gtg gtc aaa	954

Ser	Asp	Arg	Tyr	His	Glu	Gln	Val	Ser	Ala	Lys	Arg	Lys	Val	Val	Lys		
		235					240						245				
atg	atg	att	gtc	gtg	gtg	tgc	acc	ttc	gcc	atc	tgc	tgg	ctg	ccc	ttc	1002	
Met	Met	Ile	Val	Val	Val	Cys	Thr	Phe	Ala	Ile	Cys	Trp	Leu	Pro	Phe		
		250				255					260						
cac	atc	ttc	ttc	ctc	ctg	ccc	tac	atc	aac	cca	gat	ctc	tac	ctg	aag	1050	
His	Ile	Phe	Phe	Leu	Leu	Pro	Tyr	Ile	Asn	Pro	Asp	Leu	Tyr	Leu	Lys		
265					270					275					280		
aag	ttt	atc	cag	cag	gtc	tac	ctg	gcc	atc	atg	tgg	ctg	gcc	atg	agc	1098	
Lys	Phe	Ile	Gln	Gln	Val	Tyr	Leu	Ala	Ile	Met	Trp	Leu	Ala	Met	Ser		
				285					290						295		
tcc	acc	atg	tac	aac	ccc	atc	atc	tac	tgc	tgc	ctc	aat	gac	agg	ttc	1146	
Ser	Thr	Met	Tyr	Asn	Pro	Ile	Ile	Tyr	Cys	Cys	Leu	Asn	Asp	Arg	Phe		
			300					305					310				
cgt	ctg	ggc	ttc	aag	cat	gcc	ttc	cgg	tgc	tgc	ccc	ttc	atc	agc	gcc	1194	
Arg	Leu	Gly	Phe	Lys	His	Ala	Phe	Arg	Cys	Cys	Pro	Phe	Ile	Ser	Ala		
		315					320					325					
ggc	gac	tat	gag	ggg	ctg	gaa	atg	aaa	tcc	acc	cgg	tat	ctc	cag	acc	1242	
Gly	Asp	Tyr	Glu	Gly	Leu	Glu	Met	Lys	Ser	Thr	Arg	Tyr	Leu	Gln	Thr		
		330				335					340						
cag	ggc	agt	gtg	tac	aaa	gtc	agc	cgc	ctg	gag	acc	acc	atc	tcc	aca	1290	
Gln	Gly	Ser	Val	Tyr	Lys	Val	Ser	Arg	Leu	Glu	Thr	Thr	Ile	Ser	Thr		
345					350					355					360		
gtg	gtg	ggg	gcc	cac	gag	gag	gag	cca	gag	gac	ggc	ccc	aag	gcc	aca	1338	
Val	Val	Gly	Ala	His	Glu	Glu	Glu	Pro	Glu	Asp	Gly	Pro	Lys	Ala	Thr		
				365					370					375			
ccc	tgc	tcc	ctg	gac	ctg	acc	tcc	aac	tgc	tct	tca	cga	agt	gac	tcc	1386	
Pro	Ser	Ser	Leu	Asp	Leu	Thr	Ser	Asn	Cys	Ser	Ser	Arg	Ser	Asp	Ser		
			380					385					390				
aag	acc	atg	aca	gag	agc	ttc	agc	ttc	tcc	tcc	aat	gtg	ctc	tcc		1431	
Lys	Thr	Met	Thr	Glu	Ser	Phe	Ser	Phe	Ser	Ser	Asn	Val	Leu	Ser			
		395					400					405					
taggccacag	ggccttttggc	aggtgcagcc	cccactgcct	ttgacctgcc	tcccttcattg											1491	
catggaaatt	cccttcattct	ggaaccatca	gaaacaccct	cacactggga	cttgcaaaaa											1551	
gggtcagtat	gggttaggga	aaacattoca	tccttgagtc	aaaaaatctc	aattcttccc											1611	
tatctttgcc	accctcatgc	tgtgtgactc	aaaccaaatac	actgaacttt	gctgagcctg											1671	
taaaataaaa	ggtcggacca	gcttttctctc	aagagcccaa	tgcattccat	ttctggaagt											1731	
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<400> 14

Met Asp Asn Val Leu Pro Val Asp Ser Asp Leu Ser Pro Asn Ile Ser  
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Thr Asn Thr Ser Glu Pro Asn Gln Phe Val Gln Pro Ala Trp Gln Ile  
 20 25 30

Val Leu Trp Ala Ala Ala Tyr Thr Val Ile Val Val Thr Ser Val Val  
 35 40 45

Gly Asn Val Val Val Met Trp Ile Ile Leu Ala His Lys Arg Met Arg  
 50 55 60

Thr Val Thr Asn Tyr Phe Leu Val Asn Leu Ala Phe Ala Glu Ala Ser  
 65 70 75 80

Met Ala Ala Phe Asn Thr Val Val Asn Phe Thr Tyr Ala Val His Asn  
 85 90 95

Glu Trp Tyr Tyr Gly Leu Phe Tyr Cys Lys Phe His Asn Phe Phe Pro  
 100 105 110

Ile Ala Ala Val Phe Ala Ser Ile Tyr Ser Met Thr Ala Val Ala Phe  
 115 120 125

Asp Arg Tyr Met Ala Ile Ile His Pro Leu Gln Pro Arg Leu Ser Ala  
 130 135 140

Thr Ala Thr Lys Val Val Ile Cys Val Ile Trp Val Leu Ala Leu Leu  
 145 150 155 160

Leu Ala Phe Pro Gln Gly Tyr Tyr Ser Thr Thr Glu Thr Met Pro Ser  
 165 170 175

Arg Val Val Cys Met Ile Glu Trp Pro Glu His Pro Asn Lys Ile Tyr  
 180 185 190

Glu Lys Val Tyr His Ile Cys Val Thr Val Leu Ile Tyr Phe Leu Pro  
 195 200 205

Leu Leu Val Ile Gly Tyr Ala Tyr Thr Val Val Gly Ile Thr Leu Trp  
 210 215 220

Ala Ser Glu Ile Pro Gly Asp Ser Ser Asp Arg Tyr His Glu Gln Val  
 225 230 235 240

Ser Ala Lys Arg Lys Val Val Lys Met Met Ile Val Val Val Cys Thr  
 245 250 255

Phe Ala Ile Cys Trp Leu Pro Phe His Ile Phe Phe Leu Leu Pro Tyr  
 260 265 270

Ile Asn Pro Asp Leu Tyr Leu Lys Lys Phe Ile Gln Gln Val Tyr Leu  
 275 280 285

Ala Ile Met Trp Leu Ala Met Ser Ser Thr Met Tyr Asn Pro Ile Ile  
 290 295 300

Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Gly Phe Lys His Ala Phe  
 305 310 315 320

Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu Gly Leu Glu Met  
 325 330 335

Lys Ser Thr Arg Tyr Leu Gln Thr Gln Gly Ser Val Tyr Lys Val Ser  
 340 345 350

Arg Leu Glu Thr Thr Ile Ser Thr Val Val Gly Ala His Glu Glu Glu  
 355 360 365

Pro Glu Asp Gly Pro Lys Ala Thr Pro Ser Ser Leu Asp Leu Thr Ser  
 370 375 380

Asn Cys Ser Ser Arg Ser Asp Ser Lys Thr Met Thr Glu Ser Phe Ser  
 385 390 395 400

Phe Ser Ser Asn Val Leu Ser  
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<222> (211)..(1431)

<400> 15

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agaaggaccc tgagccccag gcgccagcca caggactctg ctgcagaggg gggttgtgta 180

cagatagtag gctttacgcc tagcttcgaa atg gat aac gtc ctc ccg gtg gac 234  
Met Asp Asn Val Leu Pro Val Asp  
1 5

tca gac ctc tcc cca aac atc tcc act aac acc tcg gaa ccc aat cag 282  
Ser Asp Leu Ser Pro Asn Ile Ser Thr Asn Thr Ser Glu Pro Asn Gln  
10 15 20

ttc gtg caa cca gcc tgg caa att gtc ctt tgg gca gct gcc tac acg 330  
Phe Val Gln Pro Ala Trp Gln Ile Val Leu Trp Ala Ala Ala Tyr Thr  
25 30 35 40

gtc att gtg gtg acc tct gtg gtg ggc aac gtg gta gtg atg tgg atc 378  
Val Ile Val Val Thr Ser Val Val Gly Asn Val Val Val Met Trp Ile  
45 50 55

atc tta gcc cac aaa aga atg agg aca gtg acg aac tat ttt ctg gtg 426  
Ile Leu Ala His Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Leu Val  
60 65 70

aac ctg gcc ttc gcg gag gcc tcc atg gct gca ttc aat aca gtg gtg 474  
Asn Leu Ala Phe Ala Glu Ala Ser Met Ala Ala Phe Asn Thr Val Val  
75 80 85

aac ttc acc tat gct gtc cac aac gaa tgg tac tac ggc ctg ttc tac 522  
Asn Phe Thr Tyr Ala Val His Asn Glu Trp Tyr Tyr Gly Leu Phe Tyr  
90 95 100

tgc aag ttc cac aac ttc ttc ccc atc gcc gct gtc ttc gcc agt atc 570  
Cys Lys Phe His Asn Phe Phe Pro Ile Ala Val Phe Ala Ser Ile  
105 110 115 120

tac tcc atg acg gct gtg gcc ttt gat agg tac atg gcc atc ata cat 618  
Tyr Ser Met Thr Ala Val Ala Phe Asp Arg Tyr Met Ala Ile Ile His  
125 130 135

ccc ctc cag ccc cgg ctg tca gcc aca gcc acc aaa gtg gtc atc tgt 666  
Pro Leu Gln Pro Arg Leu Ser Ala Thr Ala Thr Lys Val Val Ile Cys  
140 145 150

gtc atc tgg gtc ctg gct ctc ctg ctg gcc ttc ccc cag ggc tac tac 714  
Val Ile Trp Val Leu Ala Leu Leu Leu Ala Phe Pro Gln Gly Tyr Tyr  
155 160 165

tca acc aca gag acc atg ccc agc aga gtc gtg tgc atg atc gaa tgg 762



Ser	Thr	Thr	Glu	Thr	Met	Pro	Ser	Arg	Val	Val	Cys	Met	Ile	Glu	Trp	
170						175					180					
cca	gag	cat	ccg	aac	aag	att	tat	gag	aaa	gtg	tac	cac	atc	tgt	gtg	810
Pro	Glu	His	Pro	Asn	Lys	Ile	Tyr	Glu	Lys	Val	Tyr	His	Ile	Cys	Val	
185					190					195					200	
act	gtg	ctg	atc	tac	ttc	ctc	ccc	ctg	ctg	gtg	att	ggc	tat	gca	tac	858
Thr	Val	Leu	Ile	Tyr	Phe	Leu	Pro	Leu	Leu	Val	Ile	Gly	Tyr	Ala	Tyr	
				205						210				215		
acc	gta	gtg	gga	atc	aca	cta	tgg	gcc	agt	gag	atc	ccc	ggg	gac	tcc	906
Thr	Val	Val	Gly	Ile	Thr	Leu	Trp	Ala	Ser	Glu	Ile	Pro	Gly	Asp	Ser	
			220					225					230			
tct	gac	cgc	tac	cac	gag	caa	gtc	tct	gcc	aag	cgc	aag	gtg	gtc	aaa	954
Ser	Asp	Arg	Tyr	His	Glu	Gln	Val	Ser	Ala	Lys	Arg	Lys	Val	Val	Lys	
		235					240					245				
atg	atg	att	gtc	gtg	gtg	tgc	acc	ttc	gcc	atc	tgc	tgg	ctg	ccc	ttc	1002
Met	Met	Ile	Val	Val	Val	Cys	Thr	Phe	Ala	Ile	Cys	Trp	Leu	Pro	Phe	
		250				255					260					
cac	atc	ttc	ttc	ctc	ctg	ccc	tac	atc	aac	cca	gat	ctc	tac	ctg	aag	1050
His	Ile	Phe	Phe	Leu	Leu	Pro	Tyr	Ile	Asn	Pro	Asp	Leu	Tyr	Leu	Lys	
		265			270					275					280	
aag	ttt	atc	cag	cag	gtc	tac	ctg	gcc	atc	atg	tgg	ctg	gcc	atg	agc	1098
Lys	Phe	Ile	Gln	Gln	Val	Tyr	Leu	Ala	Ile	Met	Trp	Leu	Ala	Met	Ser	
				285					290					295		
tcc	acc	atg	tac	aac	ccc	atc	atc	tac	tgc	tgc	ctc	aat	gac	agg	ttc	1146
Ser	Thr	Met	Tyr	Asn	Pro	Ile	Ile	Tyr	Cys	Cys	Leu	Asn	Asp	Arg	Phe	
			300					305					310			
cgt	ctg	ggc	ttc	aag	cat	gcc	ttc	cgg	tgc	tgc	ccc	ttc	atc	agc	gcc	1194
Arg	Leu	Gly	Phe	Lys	His	Ala	Phe	Arg	Cys	Cys	Pro	Phe	Ile	Ser	Ala	
		315					320					325				
ggc	gac	tat	gag	ggg	ctg	gaa	atg	aaa	tcc	acc	cgg	tat	ctc	cag	acc	1242
Gly	Asp	Tyr	Glu	Gly	Leu	Glu	Met	Lys	Ser	Thr	Arg	Tyr	Leu	Gln	Thr	
		330				335					340					
cag	ggc	agt	gtg	tac	aaa	gtc	agc	cgc	ctg	gag	acc	acc	atc	tcc	aca	1290
Gln	Gly	Ser	Val	Tyr	Lys	Val	Ser	Arg	Leu	Glu	Thr	Thr	Ile	Ser	Thr	
					350					355					360	
gtg	gtg	ggg	gcc	cac	gag	gag	gag	cca	gag	gac	ggc	ccc	aag	gcc	aca	1338
Val	Val	Gly	Ala	His	Glu	Glu	Glu	Pro	Glu	Asp	Gly	Pro	Lys	Ala	Thr	
				365					370					375		
ccc	tgc	tcc	ctg	gac	ctg	acc	tcc	aac	tgc	tct	tca	cga	agt	gac	tcc	1386
Pro	Ser	Ser	Leu	Asp	Leu	Thr	Ser	Asn	Cys	Ser	Ser	Arg	Ser	Asp	Ser	
			380					385					390			
aag	acc	atg	aca	gag	agc	ttc	agc	ttc	tcc	tcc	aat	gtg	ctc	tcc		1431
Lys	Thr	Met	Thr	Glu	Ser	Phe	Ser	Phe	Ser	Ser	Asn	Val	Leu	Ser		

395

400

405

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tagggccacag ggcctttggc aggtgcagcc cccactgcct ttgacctgcc tcccttcatg 1491
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tatcttttggc accctcatgc tgtgtgactc aaaccaaadc actgaacttt gctgagcctg 1671
taaaataaaaa ggtcggacca gcttttcttc aagagcccaa tgcattccat ttctggaagt 1731
gactttggct gcatgcgagt gctcatttca ggatg 1766

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&lt;210&gt; 16

&lt;211&gt; 407

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 16

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Met Asp Asn Val Leu Pro Val Asp Ser Asp Leu Ser Pro Asn Ile Ser
1          5          10          15

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Thr Asn Thr Ser Glu Pro Asn Gln Phe Val Gln Pro Ala Trp Gln Ile
          20          25          30

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Val Leu Trp Ala Ala Ala Tyr Thr Val Ile Val Val Thr Ser Val Val
          35          40          45

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Gly Asn Val Val Val Met Trp Ile Ile Leu Ala His Lys Arg Met Arg
          50          55          60

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Thr Val Thr Asn Tyr Phe Leu Val Asn Leu Ala Phe Ala Glu Ala Ser
65          70          75          80

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Met Ala Ala Phe Asn Thr Val Val Asn Phe Thr Tyr Ala Val His Asn
          85          90          95

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Glu Trp Tyr Tyr Gly Leu Phe Tyr Cys Lys Phe His Asn Phe Phe Pro
          100          105          110

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Ile Ala Ala Val Phe Ala Ser Ile Tyr Ser Met Thr Ala Val Ala Phe
          115          120          125

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Asp Arg Tyr Met Ala Ile Ile His Pro Leu Gln Pro Arg Leu Ser Ala
          130          135          140

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Thr Ala Thr Lys Val Val Ile Cys Val Ile Trp Val Leu Ala Leu Leu  
145 150 155 160

Leu Ala Phe Pro Gln Gly Tyr Tyr Ser Thr Thr Glu Thr Met Pro Ser  
165 170 175

Arg Val Val Cys Met Ile Glu Trp Pro Glu His Pro Asn Lys Ile Tyr  
180 185 190

Glu Lys Val Tyr His Ile Cys Val Thr Val Leu Ile Tyr Phe Leu Pro  
195 200 205

Leu Leu Val Ile Gly Tyr Ala Tyr Thr Val Val Gly Ile Thr Leu Trp  
210 215 220

Ala Ser Glu Ile Pro Gly Asp Ser Ser Asp Arg Tyr His Glu Gln Val  
225 230 235 240

Ser Ala Lys Arg Lys Val Val Lys Met Met Ile Val Val Val Cys Thr  
245 250 255

Phe Ala Ile Cys Trp Leu Pro Phe His Ile Phe Phe Leu Leu Pro Tyr  
260 265 270

Ile Asn Pro Asp Leu Tyr Leu Lys Lys Phe Ile Gln Gln Val Tyr Leu  
275 280 285

Ala Ile Met Trp Leu Ala Met Ser Ser Thr Met Tyr Asn Pro Ile Ile  
290 295 300

Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Gly Phe Lys His Ala Phe  
305 310 315 320

Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu Gly Leu Glu Met  
325 330 335

Lys Ser Thr Arg Tyr Leu Gln Thr Gln Gly Ser Val Tyr Lys Val Ser  
340 345 350

Arg Leu Glu Thr Thr Ile Ser Thr Val Val Gly Ala His Glu Glu Glu  
355 360 365

Pro Glu Asp Gly Pro Lys Ala Thr Pro Ser Ser Leu Asp Leu Thr Ser  
 370 375 380

Asn Cys Ser Ser Arg Ser Asp Ser Lys Thr Met Thr Glu Ser Phe Ser  
 385 390 395 400

Phe Ser Ser Asn Val Leu Ser  
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<210> 17  
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 <212> DNA  
 <213> homo sapiens

<220>  
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 <222> (211)..(1431)

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 agaaggaccc tgagccccag ggcgccagcca caggactctg ctgcagaggg gggttgtgta 180  
 cagatagtag gctttacgcc tagcttcgaa atg gat aac gtc ctc ccg gtg gac 234  
 Met Asp Asn Val Leu Pro Val Asp  
 1 5  
 tca gac ctc tcc cca aac atc tcc act aac acc tcg gaa ccc aat cag 282  
 Ser Asp Leu Ser Pro Asn Ile Ser Thr Asn Thr Ser Glu Pro Asn Gln  
 10 15 20  
 ttc gtg caa cca gcc tgg caa att gtc ctt tgg gca gct gcc tac acg 330  
 Phe Val Gln Pro Ala Trp Gln Ile Val Leu Trp Ala Ala Ala Tyr Thr  
 25 30 35 40  
 gtc att gtg gtg acc tct gtg gtg ggc aac gtg gta gtg atg tgg atc 378  
 Val Ile Val Val Thr Ser Val Val Gly Asn Val Val Val Met Trp Ile  
 45 50 55  
 atc tta gcc cac aaa aga atg agg aca gtg acg aac tat ttt ctg gtg 426  
 Ile Leu Ala His Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Leu Val  
 60 65 70  
 aac ctg gcc ttc gcg gag gcc tcc atg gct gca ttc aat aca gtg gtg 474  
 Asn Leu Ala Phe Ala Glu Ala Ser Met Ala Ala Phe Asn Thr Val Val  
 75 80 85  
 aac ttc acc tat gct gtc cac aac gaa tgg tac tac ggc ctg ttc tac 522  
 Asn Phe Thr Tyr Ala Val His Asn Glu Trp Tyr Tyr Gly Leu Phe Tyr  
 90 95 100  
 tgc aag ttc cac aac ttc ttt ccc atc gcc gct gtc ttc gcc agt atc 570





Met Ala Ala Phe Asn Thr Val Val Asn Phe Thr Tyr Ala Val His Asn  
85 90 95

Glu Trp Tyr Tyr Gly Leu Phe Tyr Cys Lys Phe His Asn Phe Phe Pro  
100 105 110

Ile Ala Ala Val Phe Ala Ser Ile Tyr Ser Met Thr Ala Val Ala Phe  
115 120 125

Asp Arg Tyr Met Ala Ile Ile His Pro Leu Gln Pro Arg Leu Ser Ala  
130 135 140

Thr Ala Thr Lys Val Val Ile Cys Val Ile Trp Val Leu Ala Leu Leu  
145 150 155 160

Leu Ala Phe Pro Gln Gly Tyr Tyr Ser Thr Thr Glu Thr Met Pro Ser  
165 170 175

Arg Val Val Cys Met Ile Glu Trp Pro Glu His Pro Asn Lys Ile Tyr  
180 185 190

Glu Lys Val Tyr His Ile Cys Val Thr Val Leu Ile Tyr Phe Leu Pro  
195 200 205

Leu Leu Val Ile Gly Tyr Ala Tyr Thr Val Val Gly Ile Thr Leu Trp  
210 215 220

Ala Ser Glu Ile Pro Gly Asp Ser Ser Asp Arg Tyr His Glu Gln Val  
225 230 235 240

Ser Ala Lys Arg Lys Val Val Lys Met Met Ile Val Val Val Cys Thr  
245 250 255

Phe Ala Ile Cys Trp Leu Pro Phe His Ile Phe Phe Leu Leu Pro Tyr  
260 265 270

Ile Asn Pro Asp Leu Tyr Leu Lys Lys Phe Ile Gln Gln Val Tyr Leu  
275 280 285

Ala Ile Met Trp Leu Ala Met Ser Ser Thr Met Tyr Asn Pro Ile Ile  
290 295 300

Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Gly Phe Lys His Ala Phe  
305 310 315 320

Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu Gly Leu Glu Met  
325 330 335

Lys Ser Thr Arg Tyr Leu Gln Thr Gln Gly Ser Val Tyr Lys Val Ser  
340 345 350

Arg Leu Glu Thr Thr Ile Ser Thr Val Val Gly Ala His Glu Glu Glu  
355 360 365

Pro Glu Asp Gly Pro Lys Ala Thr Pro Ser Ser Leu Asp Leu Thr Ser  
370 375 380

Asn Cys Ser Ser Arg Ser Asp Ser Lys Thr Met Thr Glu Ser Phe Ser  
385 390 395 400

Phe Ser Ser Asn Val Leu Ser  
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<220>  
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agaaggaccc tgagccccag ggcgccagcca caggactctg ctgcagaggg gggttgtgta 180  
cagatagtag gctttacgcc tagcttcgaa atg gat aac gtc ctc ccg gtg gac 234  
Met Asp Asn Val Leu Pro Val Asp  
1 5  
tca gac ctc tcc cca aac atc tcc act aac acc tcg gaa ccc aat cag 282  
Ser Asp Leu Ser Pro Asn Ile Ser Thr Asn Thr Ser Glu Pro Asn Gln  
10 15 20  
ttc gtg caa cca gcc tgg caa att gtc ctt tgg gca gct gcc tac acg 330  
Phe Val Gln Pro Ala Trp Gln Ile Val Leu Trp Ala Ala Ala Tyr Thr  
25 30 35 40  
gtc att gtg gtg acc tct gtg gtg ggc aac gtg gta gtg atg tgg atc 378



Val	Ile	Val	Val	Thr	Ser	Val	Val	Gly	Asn	Val	Val	Val	Met	Trp	Ile	
				45					50					55		
atc	tta	gcc	cac	aaa	aga	atg	agg	aca	gtg	acg	aac	tat	ttt	ctg	gtg	426
Ile	Leu	Ala	His	Lys	Arg	Met	Arg	Thr	Val	Thr	Asn	Tyr	Phe	Leu	Val	
			60					65					70			
aac	ctg	gcc	ttc	gcg	gag	gcc	tcc	atg	gct	gca	ttc	aat	aca	gtg	gtg	474
Asn	Leu	Ala	Phe	Ala	Glu	Ala	Ser	Met	Ala	Ala	Phe	Asn	Thr	Val	Val	
			75				80					85				
aac	ttc	acc	tat	gct	gtc	cac	aac	gaa	tgg	tac	tac	ggc	ctg	ttc	tac	522
Asn	Phe	Thr	Tyr	Ala	Val	His	Asn	Glu	Trp	Tyr	Tyr	Gly	Leu	Phe	Tyr	
	90					95					100					
tgc	aag	ttc	cac	aac	ttc	ttt	ccc	atc	gcc	gct	gtc	ttc	gcc	agt	atc	570
Cys	Lys	Phe	His	Asn	Phe	Phe	Pro	Ile	Ala	Ala	Val	Phe	Ala	Ser	Ile	
105					110						115				120	
tac	tcc	atg	acg	gct	gtg	gcc	ttt	gat	agg	tac	atg	gcc	atc	ata	cat	618
Tyr	Ser	Met	Thr	Ala	Val	Ala	Phe	Asp	Arg	Tyr	Met	Ala	Ile	Ile	His	
				125					130					135		
ccc	ctc	cag	ccc	cgg	ctg	tca	gcc	aca	gcc	acc	aaa	gtg	gtc	atc	tgt	666
Pro	Leu	Gln	Pro	Arg	Leu	Ser	Ala	Thr	Ala	Thr	Lys	Val	Val	Ile	Cys	
			140					145					150			
gtc	atc	tgg	gtc	ctg	gct	ctc	ctg	ctg	gcc	ttc	ccc	cag	ggc	tac	tac	714
Val	Ile	Trp	Val	Leu	Ala	Leu	Leu	Leu	Ala	Phe	Pro	Gln	Gly	Tyr	Tyr	
		155					160					165				
tca	acc	aca	gag	acc	atg	ccc	agc	aga	gtc	gtg	tgc	atg	atc	gaa	tgg	762
Ser	Thr	Thr	Glu	Thr	Met	Pro	Ser	Arg	Val	Val	Cys	Met	Ile	Glu	Trp	
	170					175					180					
cca	gag	cat	ccg	aac	aag	att	tat	gag	aaa	gtg	tac	cac	atc	tgt	gtg	810
Pro	Glu	His	Pro	Asn	Lys	Ile	Tyr	Glu	Lys	Val	Tyr	His	Ile	Cys	Val	
185					190					195					200	
act	gtg	ctg	atc	tac	ttc	ctc	ccc	ctg	ctg	gtg	att	ggc	tat	gca	tac	858
Thr	Val	Leu	Ile	Tyr	Phe	Leu	Pro	Leu	Leu	Val	Ile	Gly	Tyr	Ala	Tyr	
				205					210					215		
acc	gta	gtg	gga	atc	aca	cta	tgg	gcc	agt	gag	atc	ccc	ggg	gac	tcc	906
Thr	Val	Val	Gly	Ile	Thr	Leu	Trp	Ala	Ser	Glu	Ile	Pro	Gly	Asp	Ser	
			220					225					230			
tct	gac	cgc	tac	cac	gag	caa	gtc	tct	gcc	aag	cgc	aag	gtg	gtc	aaa	954
Ser	Asp	Arg	Tyr	His	Glu	Gln	Val	Ser	Ala	Lys	Arg	Lys	Val	Val	Lys	
		235					240					245				
atg	atg	att	gtc	gtg	gtg	tgc	acc	ttc								

265	270	275	280	
aag ttt atc cag cag gtc tac ctg gcc atc atg tgg ctg gcc atg agc				1098
Lys Phe Ile Gln Gln Val Tyr Leu Ala Ile Met Trp Leu Ala Met Ser				
	285	290	295	
tcc acc atg tac aac ccc atc atc tac tgc tgc ctc aat gac agg ttc				1146
Ser Thr Met Tyr Asn Pro Ile Ile Tyr Cys Cys Leu Asn Asp Arg Phe				
	300	305	310	
cgt ctg ggc ttc aag cat gcc ttc cgg tgc tgc ccc ttc atc agc gcc				1194
Arg Leu Gly Phe Lys His Ala Phe Arg Cys Cys Pro Phe Ile Ser Ala				
	315	320	325	
ggc gac tat gag ggg ctg gaa atg aaa tcc acc cgg tat ctc cag acc				1242
Gly Asp Tyr Glu Gly Leu Glu Met Lys Ser Thr Arg Tyr Leu Gln Thr				
	330	335	340	
cag ggc agt gtg tac aaa gtc agc cgc ctg gag acc acc atc tcc aca				1290
Gln Gly Ser Val Tyr Lys Val Ser Arg Leu Glu Thr Thr Ile Ser Thr				
	345	350	355	360
gtg gtg ggg gcc cac gag gag gag cca gag gac ggc ccc aag gcc aca				1338
Val Val Gly Ala His Glu Glu Glu Pro Glu Asp Gly Pro Lys Ala Thr				
	365	370	375	
ccc tca tcc ctg gac ctg acc tcc aac tgc tct tca cga agt gac tcc				1386
Pro Ser Ser Leu Asp Leu Thr Ser Asn Cys Ser Ser Arg Ser Asp Ser				
	380	385	390	
aag acc atg aca gag agc ttc agc ttc tcc tcc aat gtg ctc tcc				1431
Lys Thr Met Thr Glu Ser Phe Ser Phe Ser Ser Asn Val Leu Ser				
	395	400	405	
taggccacag ggcctttggc aggtgcagcc cccactgcct ttgacctgcc tcccttcatg				1491
catggaaatt cccttcatct ggaaccatca gaaacaccct cacactggga cttgcaaaaa				1551
gggtcagtat gggttaggga aaacattcca tccttgagtc aaaaaatctc aattcttccc				1611
tatctttgcc accctcatgc tgtgtgactc aaaccaaadc actgaacttt gctgagcctg				1671
taaaataaaaa ggtcggacca gcttttcttc aagagcccaa tgcattccat ttctggaagt				1731
gactttggct gcatgagagt gctcatttca ggatg				1766

<210> 20  
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 <212> PRT  
 <213> homo sapiens

<400> 20

Met	Asp	Asn	Val	Leu	Pro	Val	Asp	Ser	Asp	Leu	Ser	Pro	Asn	Ile	Ser
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Thr Asn Thr Ser Glu Pro Asn Gln Phe Val Gln Pro Ala Trp Gln Ile  
20 25 30

Val Leu Trp Ala Ala Ala Tyr Thr Val Ile Val Val Thr Ser Val Val  
35 40 45

Gly Asn Val Val Val Met Trp Ile Ile Leu Ala His Lys Arg Met Arg  
50 55 60

Thr Val Thr Asn Tyr Phe Leu Val Asn Leu Ala Phe Ala Glu Ala Ser  
65 70 75 80

Met Ala Ala Phe Asn Thr Val Val Asn Phe Thr Tyr Ala Val His Asn  
85 90 95

Glu Trp Tyr Tyr Gly Leu Phe Tyr Cys Lys Phe His Asn Phe Phe Pro  
100 105 110

Ile Ala Ala Val Phe Ala Ser Ile Tyr Ser Met Thr Ala Val Ala Phe  
115 120 125

Asp Arg Tyr Met Ala Ile Ile His Pro Leu Gln Pro Arg Leu Ser Ala  
130 135 140

Thr Ala Thr Lys Val Val Ile Cys Val Ile Trp Val Leu Ala Leu Leu  
145 150 155 160

Leu Ala Phe Pro Gln Gly Tyr Tyr Ser Thr Thr Glu Thr Met Pro Ser  
165 170 175

Arg Val Val Cys Met Ile Glu Trp Pro Glu His Pro Asn Lys Ile Tyr  
180 185 190

Glu Lys Val Tyr His Ile Cys Val Thr Val Leu Ile Tyr Phe Leu Pro  
195 200 205

Leu Leu Val Ile Gly Tyr Ala Tyr Thr Val Val Gly Ile Thr Leu Trp  
210 215 220

Ala Ser Glu Ile Pro Gly Asp Ser Ser Asp Arg Tyr His Glu Gln Val  
225 230 235 240

Ser Ala Lys Arg Lys Val Val Lys Met Met Ile Val Val Val Cys Thr  
 245 250 255

Phe Ala Ile Cys Trp Leu Pro Phe His Ile Phe Phe Leu Leu Pro Tyr  
 260 265 270

Ile Asn Pro Asp Leu Tyr Leu Lys Lys Phe Ile Gln Gln Val Tyr Leu  
 275 280 285

Ala Ile Met Trp Leu Ala Met Ser Ser Thr Met Tyr Asn Pro Ile Ile  
 290 295 300

Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Gly Phe Lys His Ala Phe  
 305 310 315 320

Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu Gly Leu Glu Met  
 325 330 335

Lys Ser Thr Arg Tyr Leu Gln Thr Gln Gly Ser Val Tyr Lys Val Ser  
 340 345 350

Arg Leu Glu Thr Thr Ile Ser Thr Val Val Gly Ala His Glu Glu Glu  
 355 360 365

Pro Glu Asp Gly Pro Lys Ala Thr Pro Ser Ser Leu Asp Leu Thr Ser  
 370 375 380

Asn Cys Ser Ser Arg Ser Asp Ser Lys Thr Met Thr Glu Ser Phe Ser  
 385 390 395 400

Phe Ser Ser Asn Val Leu Ser  
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<210> 21  
 <211> 1826  
 <212> DNA  
 <213> homo sapiens

<220>  
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 <222> (61)..(1560)

<400> 21  
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Met	Ala	Ser	Arg	Leu	Thr	Leu	Leu	Thr	Leu	Leu	Leu	Leu	Leu	Leu	Ala		
1				5					10						15		
ggg	gat	aga	gcc	tcc	tca	aat	cca	aat	gct	acc	agc	tcc	agc	tcc	cag		156
Gly	Asp	Arg	Ala	Ser	Ser	Asn	Pro	Asn	Ala	Thr	Ser	Ser	Ser	Ser	Gln		
			20					25					30				
gat	cca	gag	agt	ttg	caa	gac	aga	ggc	gaa	ggg	aag	gtc	gca	aca	aca		204
Asp	Pro	Glu	Ser	Leu	Gln	Asp	Arg	Gly	Glu	Gly	Lys	Val	Ala	Thr	Thr		
			35				40					45					
gtt	atc	tcc	aag	atg	cta	ttc	gtt	gaa	ccc	atc	ctg	gag	gtt	tcc	agc		252
Val	Ile	Ser	Lys	Met	Leu	Phe	Val	Glu	Pro	Ile	Leu	Glu	Val	Ser	Ser		
	50					55					60						
ttg	ccg	aca	acc	aac	tca	aca	acc	aat	tca	gcc	acc	aaa	ata	aca	gct		300
Leu	Pro	Thr	Thr	Asn	Ser	Thr	Thr	Asn	Ser	Ala	Thr	Lys	Ile	Thr	Ala		
	65				70				75						80		
aat	acc	act	gat	gaa	ccc	acc	aca	caa	ccc	acc	aca	gag	ccc	acc	acc		348
Asn	Thr	Thr	Asp	Glu	Pro	Thr	Thr	Gln	Pro	Thr	Thr	Glu	Pro	Thr	Thr		
				85				90					95				
caa	ccc	acc	atc	caa	ccc	acc	caa	cca	act	acc	cag	ctc	cca	aca	gat		396
Gln	Pro	Thr	Ile	Gln	Pro	Thr	Gln	Pro	Thr	Thr	Gln	Leu	Pro	Thr	Asp		
			100				105					110					
tct	cct	acc	cag	ccc	act	act	ggg	tcc	ttc	tgc	cca	gga	cct	gtt	act		444
Ser	Pro	Thr	Gln	Pro	Thr	Thr	Gly	Ser	Phe	Cys	Pro	Gly	Pro	Val	Thr		
			115				120					125					
ctc	tgc	tct	gac	ttg	gag	agt	cat	tca	aca	gag	gcc	gtg	ttg	ggg	gat		492
Leu	Cys	Ser	Asp	Leu	Glu	Ser	His	Ser	Thr	Glu	Ala	Val	Leu	Gly	Asp		
	130					135					140						
gct	ttg	gta	gat	ttc	tcc	ctg	aag	ctc	tac	cac	gcc	ttc	tca	gca	atg		540
Ala	Leu	Val	Asp	Phe	Ser	Leu	Lys	Leu	Tyr	His	Ala	Phe	Ser	Ala	Met		
	145				150				155						160		
aag	aag	gtg	gag	acc	aac	atg	gcc	ttt	tcc	cca	ttc	agc	atc	gcc	agc		588
Lys	Lys	Val	Glu	Thr	Asn	Met	Ala	Phe	Ser	Pro	Phe	Ser	Ile	Ala	Ser		
				165				170					175				
ctc	ctt	acc	cag	gtc	ctg	ctc	ggg	gct	ggg	cag	aac	acc	aaa	aca	aac		636
Leu	Leu	Thr	Gln	Val	Leu	Leu	Gly	Ala	Gly	Gln	Asn	Thr	Lys	Thr	Asn		
			180				185						190				
ctg	gag	agc	atc	ctc	tct	tac	ccc	aag	gac	ttc	acc	tgt	gtc	cac	cag		684
Leu	Glu	Ser	Ile	Leu	Ser	Tyr	Pro	Lys	Asp	Phe	Thr	Cys	Val	His	Gln		
			195				200					205					
gcc	ctg	aag	ggc	ttc	acg	acc	aaa	ggt	gtc	acc	tca	gtc	tct	cag	atc		732
Ala	Leu	Lys	Gly	Phe	Thr	Thr	Lys	Gly	Val	Thr	Ser	Val	Ser	Gln	Ile		
	210																

225	230															235					240					
cgg acc ctg tac agc agc agc ccc aga gtc cta agc aac aac agt gac																										828
Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp																										
	245															250					255					
gcc aac ttg gag ctc atc aac acc tgg gtg gcc aag aac acc aac aac																										876
Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn																										
	260															265					270					
aag atc agc cgg ctg cta gac agt ctg ccc tcc gat acc cgc ctt gtc																										924
Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val																										
	275															280					285					
ctc ctc aat gct atc tac ctg agt gcc aag tgg aag aca aca ttt gat																										972
Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp																										
	290															295					300					
ccc aag aaa acc aga atg gaa ccc ttt cac ttc aaa aac tca gtt ata																										1020
Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile																										
305	310															315					320					
aaa gtg ccc atg atg aat agc aag aag tac cct gtg gcc cat ttc att																										1068
Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile																										
	325															330					335					
gac caa act ttg aaa gcc aag gtg ggg cag ctg cag ctc tcc cac aat																										1116
Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn																										
	340															345					350					
ctg agt ttg gtg atc ctg gta ccc cag aac ctg aaa cat cgt ctt gaa																										1164
Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu																										
	355															360					365					
gac atg gaa cag gct ctc agc cct tot gtt ttc aag gcc atc atg gag																										1212
Asp Met Glu Gln Ala Leu Ser Ser Pro Ser Val Phe Lys Ala Ile Met Glu																										
	370															375					380					
aaa ctg gag atg tcc aag ttc cag ccc act ctc cta aca cta ccc cgc																										1260
Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg																										
385	390															395					400					
atc aaa gtg acg acc agc cag gat atg ctc tca atc atg gag aaa ttg																										1308
Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu																										
	405															410					415					
gaa ttc ttc gat ttt tct tat gac ctt aac ctg tgt ggg ctg aca gag																										1356
Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu																										
	420															425					430					
gac cca gat ctt cag gtt tct gcg atg cag cac cag aca gtg ctg gaa																										1404
Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu																										
	435															440					445					
ctg aca gag act ggg gtg gag gcg gct gca gcc tcc gcc atc tct gtg																										1452
Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ser Ala Ile Ser Val																										
	450															455					460					

gcc cgc acc ctg ctg gtc ttt gaa gtg cag cag ccc ttc ctc ttc gtg 1500  
 Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Val  
 465 470 475 480

ctc tgg gac cag cag cac aag ttc cct gtc ttc atg ggg cga gta tat 1548  
 Leu Trp Asp Gln Gln His Lys Phe Pro Val Phe Met Gly Arg Val Tyr  
 485 490 495

gac ccc agg gcc tgagacctgc aggatcaggt tagggcgagc gctacctctc 1600  
 Asp Pro Arg Ala  
 500

cagcctcagc tctcagttgc agccctgctg ctgcctgcct ggacttgccc ctgccacctc 1660

ctgcctcagg tgtccgctat ccacaaaaag ggctcctgag ggtctgggca agggacctgc 1720

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ctagttcaag ttcaccagac tctataaata aaacctgaca gaccat 1826

<210> 22  
 <211> 500  
 <212> PRT  
 <213> homo sapiens

<400> 22

Met Ala Ser Arg Leu Thr Leu Leu Thr Leu Leu Leu Leu Leu Ala  
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Gly Asp Arg Ala Ser Ser Asn Pro Asn Ala Thr Ser Ser Ser Ser Gln  
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Asp Pro Glu Ser Leu Gln Asp Arg Gly Glu Gly Lys Val Ala Thr Thr  
 35 40 45

Val Ile Ser Lys Met Leu Phe Val Glu Pro Ile Leu Glu Val Ser Ser  
 50 55 60

Leu Pro Thr Thr Asn Ser Thr Thr Asn Ser Ala Thr Lys Ile Thr Ala  
 65 70 75 80

Asn Thr Thr Asp Glu Pro Thr Thr Gln Pro Thr Thr Glu Pro Thr Thr  
 85 90 95

Gln Pro Thr Ile Gln Pro Thr Gln Pro Thr Thr Gln Leu Pro Thr Asp  
 100 105 110

Ser Pro Thr Gln Pro Thr Thr Gly Ser Phe Cys Pro Gly Pro Val Thr  
 115 120 125

Leu Cys Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp  
 130 135 140

Ala Leu Val Asp Phe Ser Leu Lys Leu Tyr His Ala Phe Ser Ala Met  
 145 150 155 160

Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser  
 165 170 175

Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Gln Asn Thr Lys Thr Asn  
 180 185 190

Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln  
 195 200 205

Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile  
 210 215 220

Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser  
 225 230 235 240

Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp  
 245 250 255

Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn  
 260 265 270

Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val  
 275 280 285

Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp  
 290 295 300

Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile  
 305 310 315 320

Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile  
 325 330 335

Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn



340

345

350

Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu  
355 360 365

Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu  
370 375 380

Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg  
385 390 395 400

Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu  
405 410 415

Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu  
420 425 430

Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu  
435 440 445

Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ala Ser Ala Ile Ser Val  
450 455 460

Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Val  
465 470 475 480

Leu Trp Asp Gln Gln His Lys Phe Pro Val Phe Met Gly Arg Val Tyr  
485 490 495

Asp Pro Arg Ala  
500

<210> 23  
<211> 1826  
<212> DNA  
<213> homo sapiens

<220>  
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<222> (61)..(1560)

<400> 23  
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Met Ala Ser Arg Leu Thr Leu Leu Thr Leu Leu Leu Leu Leu Ala

1	5	10	15	
ggg gat aga gcc tcc tca aat cca aat gct acc agc tcc agc tcc cag				156
Gly Asp Arg Ala Ser Ser Asn Pro Asn Ala Thr Ser Ser Ser Ser Gln	20	25	30	
gat cca gag agt ttg caa gac aga ggc gaa ggg aag gtc gca aca aca				204
Asp Pro Glu Ser Leu Gln Asp Arg Gly Glu Gly Lys Val Ala Thr Thr	35	40	45	
gtt atc tcc aag atg cta ttc gtt gaa ccc atc ctg gag gtt tcc agc				252
Val Ile Ser Lys Met Leu Phe Val Glu Pro Ile Leu Glu Val Ser Ser	50	55	60	
ttg ccg aca acc aac tca aca acc aat tca gcc acc aaa ata aca gct				300
Leu Pro Thr Thr Asn Ser Thr Thr Asn Ser Ala Thr Lys Ile Thr Ala	65	70	75	80
aat acc act gat gaa ccc acc aca caa ccc acc aca gag ccc acc acc				348
Asn Thr Thr Asp Glu Pro Thr Thr Gln Pro Thr Thr Glu Pro Thr Thr	85	90	95	
caa ccc acc atc caa ccc acc caa cca act acc cag ctc cca aca gat				396
Gln Pro Thr Ile Gln Pro Thr Gln Pro Thr Thr Gln Leu Pro Thr Asp	100	105	110	
tct cct acc cag ccc act act ggg tcc ttc tgc cca gga cct gtt act				444
Ser Pro Thr Gln Pro Thr Thr Gly Ser Phe Cys Pro Gly Pro Val Thr	115	120	125	
ctc tgc tct gac ttg gag agt cat tca aca gag gcc gtg ttg ggg gat				492
Leu Cys Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp	130	135	140	
gct ttg gta gat ttc tcc ctg aag ctc tac cac gcc ttc tca gca atg				540
Ala Leu Val Asp Phe Ser Leu Lys Leu Tyr His Ala Phe Ser Ala Met	145	150	155	160
aag aag gtg gag acc aac atg gcc ttt tcc cca ttc agc atc gcc agc				588
Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser	165	170	175	
ctc ctt acc cag gtc ctg ctc ggg gct ggg cag aac acc aaa aca aac				636
Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Gln Asn Thr Lys Thr Asn	180	185	190	
ctg gag agc atc ctc tct tac ccc aag gac ttc acc tgt gtc cac cag				684
Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln	195	200	205	
gcc ctg aag ggc ttc acg acc aaa ggt gtc acc tca gtc tct cag atc				732
Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile	210	215	220	
ttc cac agc cca gac ctg gcc ata agg gac acc ttt gtg aat gcc tct				780
Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser	225	230	235	240

cgg acc ctg tac agc agc agc ccc aga gtc cta agc aac aac agt gac	828
Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp	
245 250 255	
gcc aac ttg gag ctc atc aac acc tgg gtg gcc aag aac acc aac aac	876
Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn	
260 265 270	
aag atc agc cgg ctg cta gac agt ctg ccc tcc gat acc cgc ctt gtc	924
Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val	
275 280 285	
ctc ctc aat gct atc tac ctg agt gcc aag tgg aag aca aca ttt gat	972
Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp	
290 295 300	
ccc aag aaa acc aga atg gaa ccc ttt cac ttc aaa aac tca gtt ata	1020
Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile	
305 310 315 320	
aaa gtg ccc atg atg aat agc aag aag tac cct gtg gcc cat ttc att	1068
Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile	
325 330 335	
gac caa act ttg aaa gcc aag gtg ggg cag ctg cag ctc tcc cac aat	1116
Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn	
340 345 350	
ctg agt ttg gtg atc ctg gta ccc cag aac ctg aaa cat cgt ctt gaa	1164
Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu	
355 360 365	
gac atg gaa cag gct ctc agc cct tct gtt ttc aag gcc atc atg gag	1212
Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu	
370 375 380	
aaa ctg gag atg tcc aag ttc cag ccc act ctc cta aca cta ccc cgc	1260
Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg	
385 390 395 400	
atc aaa gtg acg acc agt cag gat atg ctc tca atc atg gag aaa ttg	1308
Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu	
405 410 415	
gaa ttc ttc gat ttt tct tat gac ctt aac ctg tgt ggg ctg aca gag	1356
Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu	
420 425 430	
gac cca gat ctt cag gtt tct gcg atg cag cac cag aca gtg ctg gaa	1404
Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu	
435 440 445	
ctg aca gag act ggg gtg gag gcg gct gca gcc tcc gcc atc tct gtg	1452
Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ser Ala Ile Ser Val	
450 455 460	

gcc cgc acc ctg ctg gtc ttt gaa gtg cag cag ccc ttc ctc ttc gtg 1500  
 Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Val  
 465 470 475 480

ctc tgg gac cag cag cac aag ttc cct gtc ttc atg ggg cga gta tat 1548  
 Leu Trp Asp Gln Gln His Lys Phe Pro Val Phe Met Gly Arg Val Tyr  
 485 490 495

gac ccc agg gcc tgagacctgc aggatcaggt tagggcgagc gctacctctc 1600  
 Asp Pro Arg Ala  
 500

cagcctcagc tctcagttgc agccctgctg ctgcctgcct ggacttgccc ctgccacctc 1660

ctgcctcagg tgtccgctat ccaccaaag ggctcctgag ggtctgggca agggacctgc 1720

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ctagttcaag ttcaccagac tctataaata aaacctgaca gaccat 1826

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 <212> PRT  
 <213> homo sapiens

<400> 24

Met Ala Ser Arg Leu Thr Leu Leu Thr Leu Leu Leu Leu Leu Leu Ala  
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Gly Asp Arg Ala Ser Ser Asn Pro Asn Ala Thr Ser Ser Ser Ser Gln  
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Asp Pro Glu Ser Leu Gln Asp Arg Gly Glu Gly Lys Val Ala Thr Thr  
 35 40 45

Val Ile Ser Lys Met Leu Phe Val Glu Pro Ile Leu Glu Val Ser Ser  
 50 55 60

Leu Pro Thr Thr Asn Ser Thr Thr Asn Ser Ala Thr Lys Ile Thr Ala  
 65 70 75 80

Asn Thr Thr Asp Glu Pro Thr Thr Gln Pro Thr Thr Glu Pro Thr Thr  
 85 90 95

Gln Pro Thr Ile Gln Pro Thr Gln Pro Thr Thr Gln Leu Pro Thr Asp  
 100 105 110

Ser Pro Thr Gln Pro Thr Thr Gly Ser Phe Cys Pro Gly Pro Val Thr

115

120

125

Leu Cys Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp  
 130 135 140

Ala Leu Val Asp Phe Ser Leu Lys Leu Tyr His Ala Phe Ser Ala Met  
 145 150 155 160

Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser  
 165 170 175

Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Gln Asn Thr Lys Thr Asn  
 180 185 190

Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln  
 195 200 205

Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile  
 210 215 220

Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser  
 225 230 235 240

Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp  
 245 250 255

Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn  
 260 265 270

Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val  
 275 280 285

Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp  
 290 295 300

Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile  
 305 310 315 320

Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile  
 325 330 335

Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn  
 340 345 350

Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu  
 355 360 365

Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu  
 370 375 380

Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg  
 385 390 395 400

Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu  
 405 410 415

Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu  
 420 425 430

Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu  
 435 440 445

Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ala Ser Ala Ile Ser Val  
 450 455 460

Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Val  
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Leu Trp Asp Gln Gln His Lys Phe Pro Val Phe Met Gly Arg Val Tyr  
 485 490 495

Asp Pro Arg Ala  
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<210> 25  
 <211> 1826  
 <212> DNA  
 <213> homo sapiens

<220>  
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 <222> (61)..(1560)

<400> 25  
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 Met Ala Ser Arg Leu Thr Leu Leu Thr Leu Leu Leu Leu Leu Ala  
 1 5 10 15

ggg gat aga gcc tcc tca aat cca aat gct acc agc tcc agc tcc cag	156
Gly Asp Arg Ala Ser Ser Asn Pro Asn Ala Thr Ser Ser Ser Ser Gln	
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gat cca gag agt ttg caa gac aga ggc gaa ggg aag gtc gca aca aca	204
Asp Pro Glu Ser Leu Gln Asp Arg Gly Glu Gly Lys Val Ala Thr Thr	
35 40 45	
gtt atc tcc aag atg cta ttc gct gaa ccc atc ctg gag gtt tcc agc	252
Val Ile Ser Lys Met Leu Phe Ala Glu Pro Ile Leu Glu Val Ser Ser	
50 55 60	
ttg ccg aca acc aac tca aca acc aat tca gcc acc aaa ata aca gct	300
Leu Pro Thr Thr Asn Ser Thr Thr Asn Ser Ala Thr Lys Ile Thr Ala	
65 70 75 80	
aat acc act gat gaa ccc acc aca caa ccc acc aca gag ccc acc acc	348
Asn Thr Thr Asp Glu Pro Thr Thr Gln Pro Thr Thr Glu Pro Thr Thr	
85 90 95	
caa ccc acc atc caa ccc acc caa cca act acc cag ctc cca aca gat	396
Gln Pro Thr Ile Gln Pro Thr Gln Pro Thr Thr Gln Leu Pro Thr Asp	
100 105 110	
tct cct acc cag ccc act act ggg tcc ttc tgc cca gga cct gtt act	444
Ser Pro Thr Gln Pro Thr Thr Gly Ser Phe Cys Pro Gly Pro Val Thr	
115 120 125	
ctc tgc tct gac ttg gag agt cat tca aca gag gcc gtg ttg ggg gat	492
Leu Cys Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp	
130 135 140	
gct ttg gta gat ttc tcc ctg aag ctc tac cac gcc ttc tca gca atg	540
Ala Leu Val Asp Phe Ser Leu Lys Leu Tyr His Ala Phe Ser Ala Met	
145 150 155 160	
aag aag gtg gag acc aac atg gcc ttt tcc cca ttc agc atc gcc agc	588
Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser	
165 170 175	
ctc ctt acc cag gtc ctg ctc ggg gct ggg cag aac acc aaa aca aac	636
Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Gln Asn Thr Lys Thr Asn	
180 185 190	
ctg gag agc atc ctc tct tac ccc aag gac ttc acc tgt gtc cac cag	684
Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln	
195 200 205	
gcc ctg aag ggc ttc acg acc aaa ggt gtc acc tca gtc tct cag atc	732
Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile	
210 215 220	
ttc cac agc cca gac ctg gcc ata agg gac acc ttt gtg aat gcc tct	780
Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser	
225 230 235 240	

cgg acc ctg tac agc agc agc ccc aga gtc cta agc aac aac agt gac	828
Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp	
245 250 255	
gcc aac ttg gag ctc atc aac acc tgg gtg gcc aag aac acc aac aac	876
Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn	
260 265 270	
aag atc agc cgg ctg cta gac agt ctg ccc tcc gat acc cgc ctt gtc	924
Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val	
275 280 285	
ctc ctc aat gct atc tac ctg agt gcc aag tgg aag aca aca ttt gat	972
Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp	
290 295 300	
ccc aag aaa acc aga atg gaa ccc ttt cac ttc aaa aac tca gtt ata	1020
Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile	
305 310 315 320	
aaa gtg ccc atg atg aat agc aag aag tac cct gtg gcc cat ttc att	1068
Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile	
325 330 335	
gac caa act ttg aaa gcc aag gtg ggg cag ctg cag ctc tcc cac aat	1116
Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn	
340 345 350	
ctg agt ttg gtg atc ctg gta ccc cag aac ctg aaa cat cgt ctt gaa	1164
Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu	
355 360 365	
gac atg gaa cag gct ctc agc cct tct gtt ttc aag gcc atc atg gag	1212
Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu	
370 375 380	
aaa ctg gag atg tcc aag ttc cag ccc act ctc cta aca cta ccc cgc	1260
Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg	
385 390 395 400	
atc aaa gtg acg acc agc cag gat atg ctc tca atc atg gag aaa ttg	1308
Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu	
405 410 415	
gaa ttc ttc gat ttt tct tat gac ctt aac ctg tgt ggg ctg aca gag	1356
Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu	
420 425 430	
gac cca gat ctt cag gtt tct gcg atg cag cac cag aca gtg ctg gaa	1404
Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu	
435 440 445	
ctg aca gag act ggg gtg gag gcg gct gca gcc tcc gcc atc tct gtg	1452
Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ser Ala Ile Ser Val	
450 455 460	
gcc cgc acc ctg ctg gtc ttt gaa gtg cag cag ccc ttc ctc ttc gtg	1500





Leu Cys Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp  
130 135 140

Ala Leu Val Asp Phe Ser Leu Lys Leu Tyr His Ala Phe Ser Ala Met  
145 150 155 160

Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser  
165 170 175

Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Gln Asn Thr Lys Thr Asn  
180 185 190

Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln  
195 200 205

Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile  
210 215 220

Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser  
225 230 235 240

Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp  
245 250 255

Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn  
260 265 270

Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val  
275 280 285

Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp  
290 295 300

Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile  
305 310 315 320

Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile  
325 330 335

Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn  
340 345 350

Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu  
 355 360 365

Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu  
 370 375 380

Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg  
 385 390 395 400

Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu  
 405 410 415

Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu  
 420 425 430

Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu  
 435 440 445

Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ala Ser Ala Ile Ser Val  
 450 455 460

Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Val  
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Asp Pro Arg Ala  
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<220>  
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 Met Ala Ser Arg Leu Thr Leu Leu Thr Leu Leu Leu Leu Leu Ala  
 1 5 10 15



Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp	
245 250 255	
gcc aac ttg gag ctc atc aac acc tgg gtg gcc aag aac acc aac aac	876
Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn	
260 265 270	
aag atc agc cgg ctg cta gac agt ctg ccc tcc gat acc cgc ctt gtc	924
Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val	
275 280 285	
ctc ctc aat gct atc tac ctg agt gcc aag tgg aag aca aca ttt gat	972
Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp	
290 295 300	
ccc aag aaa acc aga atg gaa ccc ttt cac ttc aaa aac tca gtt ata	1020
Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile	
305 310 315 320	
aaa gtg ccc atg atg aat agc aag aag tac cct gtg gcc cat ttc att	1068
Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile	
325 330 335	
gac caa act ttg aaa gcc aag gtg ggg cag ctg cag ctc tcc cac aat	1116
Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn	
340 345 350	
ctg agt ttg gtg atc ctg gta ccc cag aac ctg aaa cat cgt ctt gaa	1164
Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu	
355 360 365	
gac atg gaa cag gct ctc agc cct tct gtt ttc aag gcc atc atg gag	1212
Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu	
370 375 380	
aaa ctg gag atg tcc aag ttc cag ccc act ctc cta aca cta ccc cgc	1260
Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg	
385 390 395 400	
atc aaa gtg acg acc agc cag gat atg ctc tca atc atg gag aaa ttg	1308
Ile Lys Val Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu	
405 410 415	
gaa ttc ttc gat ttt tct tat gac ctt aac ctg tgt ggg ctg aca gag	1356
Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu	
420 425 430	
gac cca gat ctt cag gtt tct gcg atg cag cac cag aca gtg ctg gaa	1404
Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu	
435 440 445	
ctg aca gag act ggg gtg gag gcg gct gca gcc tcc gcc atc tct gtg	1452
Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ala Ser Ala Ile Ser Val	
450 455 460	
gcc cgc acc ctg ctg gtc ttt gaa gtg cag cag ccc ttc ctc ttc gtg	1500
Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Val	

465	470	475	480	
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Leu Trp Asp Gln Gln His Lys Phe Pro Val Phe Met Gly Arg Val Tyr				
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Asp Pro Arg Ala				
	500			
cagcctcagc tctcagttgc agccctgctg ctgcctgcct ggacttgccc ctgccacctc				1660
ctgcctcagg tgtccgctat ccacaaaaag ggctcctgag ggtctgggca agggacctgc				1720
ttctattagc ccttctccat ggccctgcca tgctctccaa accacttttt gcagctttct				1780
ctagttcaag ttcaccagac tctataaata aaacctgaca gaccat				1826

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<400> 28

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Gly	Asp	Arg	Ala	Ser	Ser	Asn	Pro	Asn	Ala	Thr	Ser	Ser	Ser	Gln
			20					25					30	
Asp	Pro	Glu	Ser	Leu	Gln	Asp	Arg	Gly	Glu	Gly	Lys	Val	Ala	Thr
		35					40					45		
Val	Ile	Ser	Lys	Met	Leu	Phe	Val	Glu	Pro	Ile	Leu	Glu	Val	Ser
	50					55					60			
Leu	Pro	Thr	Thr	Asn	Ser	Thr	Thr	Asn	Ser	Ala	Thr	Lys	Ile	Thr
65					70					75				80
Asn	Thr	Thr	Asp	Glu	Pro	Thr	Thr	Gln	Pro	Thr	Thr	Glu	Pro	Thr
				85					90					95
Gln	Pro	Thr	Ile	Gln	Pro	Thr	Gln	Pro	Thr	Thr	Gln	Leu	Pro	Thr
			100					105					110	
Ser	Pro	Thr	Gln	Pro	Thr	Thr	Gly	Ser	Phe	Cys	Pro	Gly	Pro	Val
			115				120					125		

Leu Cys Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp  
130 135 140

Ala Leu Val Asp Phe Ser Leu Lys Leu Tyr His Ala Phe Ser Gly Met  
145 150 155 160

Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser  
165 170 175

Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Gln Asn Thr Lys Thr Asn  
180 185 190

Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln  
195 200 205

Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile  
210 215 220

Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser  
225 230 235 240

Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp  
245 250 255

Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn  
260 265 270

Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val  
275 280 285

Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp  
290 295 300

Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile  
305 310 315 320

Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile  
325 330 335

Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn  
340 345 350

Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu  
 355 360 365

Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu  
 370 375 380

Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg  
 385 390 395 400

Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu  
 405 410 415

Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu  
 420 425 430

Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu  
 435 440 445

Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ala Ser Ala Ile Ser Val  
 450 455 460

Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Val  
 465 470 475 480

Leu Trp Asp Gln Gln His Lys Phe Pro Val Phe Met Gly Arg Val Tyr  
 485 490 495

Asp Pro Arg Ala  
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<220>  
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 Met Ala Ser Arg Leu Thr Leu Leu Thr Leu Leu Leu Leu Leu Ala  
 1 5 10 15  
 ggg gat aga gcc tcc tca aat cca aat gct acc agc tcc agc tcc cag 156





245								250				255					
gcc	aac	ttg	gag	ctc	atc	aac	acc	tgg	gtg	gcc	aag	aac	acc	aac	aac		876
Ala	Asn	Leu	Glu	Leu	Ile	Asn	Thr	Trp	Val	Ala	Lys	Asn	Thr	Asn	Asn		
		260						265					270				
aag	atc	agc	cgg	ctg	cta	gac	agt	ctg	ccc	tcc	gat	acc	cgc	ctt	gtc		924
Lys	Ile	Ser	Arg	Leu	Leu	Asp	Ser	Leu	Pro	Ser	Asp	Thr	Arg	Leu	Val		
		275					280					285					
ctc	ctc	aat	gct	atc	tac	ctg	agt	gcc	aag	tgg	aag	aca	aca	ttt	gat		972
Leu	Leu	Asn	Ala	Ile	Tyr	Leu	Ser	Ala	Lys	Trp	Lys	Thr	Thr	Phe	Asp		
	290					295					300						
ccc	aag	aaa	acc	aga	atg	gaa	ccc	ttt	cac	ttc	aaa	aac	tca	gtt	ata		1020
Pro	Lys	Lys	Thr	Arg	Met	Glu	Pro	Phe	His	Phe	Lys	Asn	Ser	Val	Ile		
305					310					315					320		
aaa	gtg	ccc	atg	atg	aat	agc	aag	aag	tac	cct	gtg	gcc	cat	ttc	att		1068
Lys	Val	Pro	Met	Met	Asn	Ser	Lys	Lys	Tyr	Pro	Val	Ala	His	Phe	Ile		
				325					330					335			
gac	caa	act	ttg	aaa	gcc	aag	gtg	ggg	cag	ctg	cag	ctc	tcc	cac	aat		1116
Asp	Gln	Thr	Leu	Lys	Ala	Lys	Val	Gly	Gln	Leu	Gln	Leu	Ser	His	Asn		
			340					345					350				
ctg	agt	ttg	gtg	atc	ctg	gta	ccc	cag	aac	ctg	aaa	cat	cgt	ctt	gaa		1164
Leu	Ser	Leu	Val	Ile	Leu	Val	Pro	Gln	Asn	Leu	Lys	His	Arg	Leu	Glu		
		355					360					365					
gac	atg	gaa	cag	gct	ctc	agc	cct	tct	gtt	ttc	aag	gcc	atc	atg	gag		1212
Asp	Met	Glu	Gln	Ala	Leu	Ser	Pro	Ser	Val	Phe	Lys	Ala	Ile	Met	Glu		
	370					375					380						
aaa	ctg	gag	atg	tcc	aag	ttc	cag	ccc	act	ctc	cta	aca	cta	ccc	cgc		1260
Lys	Leu	Glu	Met	Ser	Lys	Phe	Gln	Pro	Thr	Leu	Leu	Thr	Leu	Pro	Arg		
385					390					395					400		
atc	aaa	gtg	acg	acc	agc	cag	gat	atg	ctc	tca	atc	atg	gag	aaa	ttg		1308
Ile	Lys	Val	Thr	Thr	Ser	Gln	Asp	Met	Leu	Ser	Ile	Met	Glu	Lys	Leu		
				405					410					415			
gaa	ttc	ttc	gat	ttt	tct	tat	gac	ctt	aac	ctg	tgt	ggg	ctg	aca	gag		1356
Glu	Phe	Phe	Asp	Phe	Ser	Tyr	Asp	Leu	Asn	Leu	Cys	Gly	Leu	Thr	Glu		
			420				425						430				
gac	cca	gat	ctt	cag	gtt	tct	gcg	atg	cag	cac	cag	aca	gtg	ctg	gaa		1404
Asp	Pro	Asp	Leu	Gln	Val	Ser	Ala	Met	Gln	His	Gln	Thr	Val	Leu	Glu		
		435					440					445					
ctg	aca	gag	act	ggg	gt												

ctc tgg gac cag cag cac aag ttc cct gtc ttc atg ggg cga gta tat 1548  
 Leu Trp Asp Gln Gln His Lys Phe Pro Val Phe Met Gly Arg Val Tyr  
                   485                  490                  495

gac ccc agg gcc tgagacctgc aggatcaggt tagggcgagc gctacctctc 1600  
 Asp Pro Arg Ala  
                   500

cagcctcagc tctcagttgc agccctgctg ctgcctgcct ggacttgccc ctgccacctc 1660

ctgcctcagg tgtccgctat ccaccaaag ggctcctgag ggtctgggca agggacctgc 1720

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<400> 30

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                   20                  25                  30

Asp Pro Glu Ser Leu Gln Asp Arg Gly Glu Gly Lys Val Ala Thr Thr  
                   35                  40                  45

Val Ile Ser Lys Met Leu Phe Val Glu Pro Ile Leu Glu Val Ser Ser  
                   50                  55                  60

Leu Pro Thr Thr Asn Ser Thr Thr Asn Ser Ala Thr Lys Ile Thr Ala  
 65                  70                  75                  80

Asn Thr Thr Asp Glu Pro Thr Thr Gln Pro Thr Thr Glu Pro Thr Thr  
                   85                  90                  95

Gln Pro Thr Ile Gln Pro Thr Gln Pro Thr Thr Gln Leu Pro Thr Asp  
                   100                  105                  110

Ser Pro Thr Gln Pro Thr Thr Gly Ser Phe Cys Pro Gly Pro Val Thr  
                   115                  120                  125

Leu Cys Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp  
130 135 140

Ala Leu Val Asp Phe Ser Leu Lys Leu Tyr His Ala Phe Ser Ala Met  
145 150 155 160

Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser  
165 170 175

Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Gln Asn Thr Lys Thr Asn  
180 185 190

Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln  
195 200 205

Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile  
210 215 220

Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser  
225 230 235 240

Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp  
245 250 255

Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn  
260 265 270

Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val  
275 280 285

Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp  
290 295 300

Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile  
305 310 315 320

Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile  
325 330 335

Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn  
340 345 350

Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu

355

360

365

Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu  
370 375 380

Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg  
385 390 395 400

Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu  
405 410 415

Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu  
420 425 430

Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu  
435 440 445

Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ala Ser Ala Ile Ser Val  
450 455 460

Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Met  
465 470 475 480

Leu Trp Asp Gln Gln His Lys Phe Pro Val Phe Met Gly Arg Val Tyr  
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Asp Pro Arg Ala  
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Met Trp Phe Leu Val Leu  
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Cys Leu Ala Leu Ser Leu Gly Gly Thr Gly Ala Ala Pro Pro Ile Gln  
10 15 20

tcc cgg att gtg gga ggc tgg gag tgt gag cag cat tcc cag ccc tgg	150
Ser Arg Ile Val Gly Gly Trp Glu Cys Glu Gln His Ser Gln Pro Trp	
25 30 35	
cag gcg gct ctg tac cat ttc agc act ttc cag tgt ggg ggc atc ctg	198
Gln Ala Ala Leu Tyr His Phe Ser Thr Phe Gln Cys Gly Gly Ile Leu	
40 45 50	
gtg cac cgc cag tgg gtg ctc aca gct gct cat tgc atc agc gac aat	246
Val His Arg Gln Trp Val Leu Thr Ala Ala His Cys Ile Ser Asp Asn	
55 60 65 70	
tac cag ctc tgg ctg ggt cgc cac aac ttg ttt gac gac gaa aac aca	294
Tyr Gln Leu Trp Leu Gly Arg His Asn Leu Phe Asp Asp Glu Asn Thr	
75 80 85	
gcc cag ttt gtt cat gtc agt gag agc ttc cca cac cct ggc ttc aac	342
Ala Gln Phe Val His Val Ser Glu Ser Phe Pro His Pro Gly Phe Asn	
90 95 100	
atg agc ctc ctg gag aac cac acc cgc caa gca gac gag gac tac agc	390
Met Ser Leu Leu Glu Asn His Thr Arg Gln Ala Asp Glu Asp Tyr Ser	
105 110 115	
cac gac ctc atg ctg ctc cgc ctg aca gag cct gct gat acc atc aca	438
His Asp Leu Met Leu Leu Arg Leu Thr Glu Pro Ala Asp Thr Ile Thr	
120 125 130	
gat gct gtg aag gtc gtg gag ttg ccc acc gag gaa ccc gaa gtg ggg	486
Asp Ala Val Lys Val Val Glu Leu Pro Thr Glu Glu Pro Glu Val Gly	
135 140 145 150	
agc acc tgt ttg gct tcc ggc tgg ggc agc atc gaa cca gag aat ttc	534
Ser Thr Cys Leu Ala Ser Gly Trp Gly Ser Ile Glu Pro Glu Asn Phe	
155 160 165	
tca ttt cca gat gat ctc cag tgt gtg gac ctc aaa atc ctg cct aat	582
Ser Phe Pro Asp Asp Leu Gln Cys Val Asp Leu Lys Ile Leu Pro Asn	
170 175 180	
gat gag tgc aaa aaa gcc cac gtc cag aag gtg aca gac ttc atg ctg	630
Asp Glu Cys Lys Lys Ala His Val Gln Lys Val Thr Asp Phe Met Leu	
185 190 195	
tgt gtc gga cac ctg gaa ggt ggc aaa gac acc tgt gtg ggt gat tca	678
Cys Val Gly His Leu Glu Gly Gly Lys Asp Thr Cys Val Gly Asp Ser	
200 205 210	
ggg ggc ccg ctg atg tgt gat ggt gtg ctc caa ggt gtc aca tca tgg	726
Gly Gly Pro Leu Met Cys Asp Gly Val Leu Gln Gly Val Thr Ser Trp	
215 220 225 230	
ggc tac gtc cct tgt ggc acc ccc aat aag cct tct gtc gcc gtc aga	774
Gly Tyr Val Pro Cys Gly Thr Pro Asn Lys Pro Ser Val Ala Val Arg	
235 240 245	
gtg ctg tct tat gtg aag tgg atc gag gac acc ata gcg gag aac tcc	822

Val Leu Ser Tyr Val Lys Trp Ile Glu Asp Thr Ile Ala Glu Asn Ser  
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871

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 <212> PRT  
 <213> homo sapiens

<400> 32

Met Trp Phe Leu Val Leu Cys Leu Ala Leu Ser Leu Gly Gly Thr Gly  
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Ala Ala Pro Pro Ile Gln Ser Arg Ile Val Gly Gly Trp Glu Cys Glu  
 20 25 30

Gln His Ser Gln Pro Trp Gln Ala Ala Leu Tyr His Phe Ser Thr Phe  
 35 40 45

Gln Cys Gly Gly Ile Leu Val His Arg Gln Trp Val Leu Thr Ala Ala  
 50 55 60

His Cys Ile Ser Asp Asn Tyr Gln Leu Trp Leu Gly Arg His Asn Leu  
 65 70 75 80

Phe Asp Asp Glu Asn Thr Ala Gln Phe Val His Val Ser Glu Ser Phe  
 85 90 95

Pro His Pro Gly Phe Asn Met Ser Leu Leu Glu Asn His Thr Arg Gln  
 100 105 110

Ala Asp Glu Asp Tyr Ser His Asp Leu Met Leu Leu Arg Leu Thr Glu  
 115 120 125

Pro Ala Asp Thr Ile Thr Asp Ala Val Lys Val Val Glu Leu Pro Thr  
 130 135 140

Glu Glu Pro Glu Val Gly Ser Thr Cys Leu Ala Ser Gly Trp Gly Ser  
 145 150 155 160

Ile Glu Pro Glu Asn Phe Ser Phe Pro Asp Asp Leu Gln Cys Val Asp  
 165 170 175

Leu Lys Ile Leu Pro Asn Asp Glu Cys Lys Lys Ala His Val Gln Lys  
 180 185 190

Val Thr Asp Phe Met Leu Cys Val Gly His Leu Glu Gly Gly Lys Asp  
 195 200 205

Thr Cys Val Gly Asp Ser Gly Gly Pro Leu Met Cys Asp Gly Val Leu  
 210 215 220

Gln Gly Val Thr Ser Trp Gly Tyr Val Pro Cys Gly Thr Pro Asn Lys  
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Pro Ser Val Ala Val Arg Val Leu Ser Tyr Val Lys Trp Ile Glu Asp  
 245 250 255

Thr Ile Ala Glu Asn Ser  
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cgctggggaa agaaaggaca aagggaatgt tggagctaca g

41

<210> 278  
<211> 41  
<212> DNA

<213> homo sapiens

<400> 278

gcggtaggaa gactgttaag gtgcatctct tattttctag g

41

<210> 279

<211> 41

<212> DNA

<213> homo sapiens

<400> 279

cgcaccaaag tgacgaccag tcaggatatg ctctcaatca t

41

<210> 280

<211> 41

<212> DNA

<213> homo sapiens

<400> 280

tatctccaag atgctattcg ctgaacccat cctggagggt t

41

<210> 281

<211> 41

<212> DNA

<213> homo sapiens

<400> 281

gctctaccac gccttctcag gaatgaagaa ggtggagacc a

41

<210> 282

<211> 41

<212> DNA

<213> homo sapiens

<400> 282

tgcagcagcc cttcctcttc atgctctggg accagcagca c

41

<210> 283

<211> 41

<212> DNA

<213> homo sapiens

<400> 283

tcctgcctaa tgatgagtgc gaaaaagccc acgtccagaa g

41

<210> 284

<211> 41

<212> DNA

<213> homo sapiens

<400> 284

cagactgtgt agcccaaggc agggatgggg actcctgcgt c

41

<210> 285  
<211> 41  
<212> DNA  
<213> homo sapiens

<400> 285  
aggtcgtgga gttgccacc caggaacccg aagtggggag c

41

<210> 286  
<211> 41  
<212> DNA  
<213> homo sapiens

<400> 286  
ggcggggatg gggactcctg tgtccaaggg agaaagggcc a

41

<210> 287  
<211> 41  
<212> DNA  
<213> homo sapiens

<400> 287  
gggccacccc agctgtgtca gtctcatgcc tggaagtctg a

41

<210> 288  
<211> 41  
<212> DNA  
<213> homo sapiens

<400> 288  
tgtcacgttc tgccatcacc catctttcca gatgtggtgc a

41

<210> 289  
<211> 1082  
<212> DNA  
<213> homo sapiens

<220>  
<221> misc\_feature  
<222> (956)..(956)  
<223> wherein N is either a "G" or an "A".

<220>  
<221> misc\_feature  
<222> (129)..(129)  
<223> wherein N is either a "T" or a "C".

<220>

<221> misc\_feature  
 <222> (348)..(348)  
 <223> wherein N is either a "C" or a "T".

<220>  
 <221> misc\_feature  
 <222> (462)..(462)  
 <223> wherein N is either a "G" or an "A".

<220>  
 <221> misc\_feature  
 <222> (577)..(577)  
 <223> wherein N is either a "C" or a "G".

<220>  
 <221> misc\_feature  
 <222> (705)..(705)  
 <223> wherein N is either a "G" or an "A".

<400> 289  
 ctgtgcatgg catcatcctg gccccctcta gagctccaat cctccaacca gagccagctc 60  
 ttccctcaaa atgctacggc ctgtgacaat gctccagaag cctgggacct gctgcacaga 120  
 gtgctgccna catttatcat ctccatctgt ttcttcggcc tcttagggaa cctttttgtc 180  
 ctgttggtct tctcctgcc ccggcggcaa ctgaacgtgg cagaaatcta cctggccaac 240  
 ctggcagcct ctgatctggt gtttgtcttg ggcttgccct tctgggcaga gaatatctgg 300  
 aaccagttta actggccttt cggagccctc ctctgccgtg tcatcaangg ggtcatcaag 360  
 gccaatttgt tcatcagcat ctctctggtg gtggccatca gccaggaccg ctaccgcgtg 420  
 ctggtgcacc ctatggccag cggaaggcag cagcggcgga gncaggcccg ggtcacctgc 480  
 gtgctcatct gggttgtggg gggcctcttg agcatcccca cattcctgct gcgatccatc 540  
 caagccgtcc cagatctgaa catcacgcc tgcactntgc tctccccca tgaggcctgg 600  
 cactttgcaa ggattgtgga gttaaatatt ctgggtttcc tctaccact ggctgcgatc 660  
 gtcttcttca actaccacat cctggcctcc ctgcgaacgc gggangaggt cagcaggaca 720  
 agagtgcngg ggccgaagga tagcaagacc acagcgctga tctcacgct cgtggttgcc 780  
 ttcttggtct gctgggcccc ttaccacttc tttgccttcc tgggaattctt attccaggtg 840  
 caagcagtcc gaggtgctt ttgggaggac ttcatlgacc tgggcctgca attggccaac 900  
 ttctttgcct tactaacag ctccctgaat ccagtaattt atgtctttgt gggccngctc 960  
 ttcaggacca aggtctggga actttataaa caatgcaccc ctaaaagtct tgctccaata 1020

tcttcatccc ataggaaaga aatcttccaa cttttctggc ggaattaaaa cagcattgaa 1080  
cc 1082

<210> 290  
<211> 353  
<212> PRT  
<213> homo sapiens

<220>  
<221> VARIANT  
<222> (317)..(317)  
<223> wherein Xaa is either "Arg" or "Gln".

<220>  
<221> VARIANT  
<222> (241)..(241)  
<223> wherein Xaa is either "Arg" or "Asn".

<220>  
<221> VARIANT  
<222> (191)..(191)  
<223> wherein Xaa is either "Leu" or "Val".

<400> 290

Met	Ala	Ser	Ser	Trp	Pro	Pro	Leu	Glu	Leu	Gln	Ser	Ser	Asn	Gln	Ser	1	5	10	15
Gln	Leu	Phe	Pro	Gln	Asn	Ala	Thr	Ala	Cys	Asp	Asn	Ala	Pro	Glu	Ala	20	25	30	
Trp	Asp	Leu	Leu	His	Arg	Val	Leu	Pro	Thr	Phe	Ile	Ile	Ser	Ile	Cys	35	40	45	
Phe	Phe	Gly	Leu	Leu	Gly	Asn	Leu	Phe	Val	Leu	Leu	Val	Phe	Leu	Leu	50	55	60	
Pro	Arg	Arg	Gln	Leu	Asn	Val	Ala	Glu	Ile	Tyr	Leu	Ala	Asn	Leu	Ala	65	70	75	80
Ala	Ser	Asp	Leu	Val	Phe	Val	Leu	Gly	Leu	Pro	Phe	Trp	Ala	Glu	Asn	85	90	95	
Ile	Trp	Asn	Gln	Phe	Asn	Trp	Pro	Phe	Gly	Ala	Leu	Leu	Cys	Arg	Val	100	105	110	
Ile	Asn	Gly	Val	Ile	Lys	Ala	Asn	Leu	Phe	Ile	Ser	Ile	Phe	Leu	Val	115	120	125	
Val	Ala	Ile	Ser	Gln	Asp	Arg	Tyr	Arg	Val	Leu	Val	His	Pro	Met	Ala	130	135	140	

Ser Gly Arg Gln Gln Arg Arg Arg Gln Ala Arg Val Thr Cys Val Leu  
 145 150 155 160  
 Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg  
 165 170 175  
 Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Xaa Leu  
 180 185 190  
 Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile  
 195 200 205  
 Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His  
 210 215 220  
 Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val  
 225 230 235 240  
 Xaa Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val  
 245 250 255  
 Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu  
 260 265 270  
 Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp  
 275 280 285  
 Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn  
 290 295 300  
 Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Xaa Leu Phe Arg  
 305 310 315 320  
 Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala  
 325 330 335  
 Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg  
 340 345 350

Asn

<210> 291  
 <211> 1766  
 <212> DNA  
 <213> homo sapiens

<220>  
 <221> CDS  
 <222> (211)..(1431)

<220>  
 <221> misc\_feature  
 <222> (543)..(543)  
 <223> wherein N is either a "T" or a "C".



<220>  
 <221> misc\_feature  
 <222> (672)..(672)  
 <223> wherein N is either a "C" or an "A".

<220>  
 <221> misc\_feature  
 <222> (1344)..(1344)  
 <223> wherein N is either a "G" or an "A".

<400> 291  
 aattcagagc caccgcggggc aggcggggcag tgcattccaga agcgtttata ttctgagcgc 60  
 cagttcagct ttcaaaaaga gtgctgcccc taaaaagcct tccaccctcc tgtctgcttt 120  
 agaaggaccc tgagccccag gcgccagcca caggactctg ctgcagaggg gggttgtgta 180  
 cagatagtag gctttacgcc tagcttcgaa atg gat aac gtc ctc ccg gtg gac 234  
 Met Asp Asn Val Leu Pro Val Asp  
 1 5  
 tca gac ctc tcc cca aac atc tcc act aac acc tcg gaa ccc aat cag 282  
 Ser Asp Leu Ser Pro Asn Ile Ser Thr Asn Thr Ser Glu Pro Asn Gln  
 10 15 20  
 ttc gtg caa cca gcc tgg caa att gtc ctt tgg gca gct gcc tac acg 330  
 Phe Val Gln Pro Ala Trp Gln Ile Val Leu Trp Ala Ala Ala Tyr Thr  
 25 30 35 40  
 gtc att gtg gtg acc tct gtg gtg ggc aac gtg gta gtg atg tgg atc 378  
 Val Ile Val Val Thr Ser Val Val Gly Asn Val Val Val Met Trp Ile  
 45 50 55  
 atc tta gcc cac aaa aga atg agg aca gtg acg aac tat ttt ctg gtg 426  
 Ile Leu Ala His Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Leu Val  
 60 65 70  
 aac ctg gcc ttc gcg gag gcc tcc atg gct gca ttc aat aca gtg gtg 474  
 Asn Leu Ala Phe Ala Glu Ala Ser Met Ala Ala Phe Asn Thr Val Val  
 75 80 85  
 aac ttc acc tat gct gtc cac aac gaa tgg tac tac ggc ctg ttc tac 522  
 Asn Phe Thr Tyr Ala Val His Asn Glu Trp Tyr Tyr Gly Leu Phe Tyr  
 90 95 100  
 tgc aag ttc cac aac ttc ttn ccc atc gcc gct gtc ttc gcc agt atc 570  
 Cys Lys Phe His Asn Phe Xaa Pro Ile Ala Ala Val Phe Ala Ser Ile  
 105 110 115 120  
 tac tcc atg acg gct gtg gcc ttt gat agg tac atg gcc atc ata cat 618  
 Tyr Ser Met Thr Ala Val Ala Phe Asp Arg Tyr Met Ala Ile Ile His  
 125 130 135  
 ccc ctc cag ccc cgg ctg tca gcc aca gcc acc aaa gtg gtc atc tgt 666

Pro	Leu	Gln	Pro	Arg	Leu	Ser	Ala	Thr	Ala	Thr	Lys	Val	Val	Ile	Cys		
			140					145					150				
gtc	atn	tgg	gtc	ctg	gct	ctc	ctg	ctg	gcc	ttc	ccc	cag	ggc	tac	tac	714	
Val	Xaa	Trp	Val	Leu	Ala	Leu	Leu	Leu	Ala	Phe	Pro	Gln	Gly	Tyr	Tyr		
		155					160					165					
tca	acc	aca	gag	acc	atg	ccc	agc	aga	gtc	gtg	tgc	atg	atc	gaa	tgg	762	
Ser	Thr	Thr	Glu	Thr	Met	Pro	Ser	Arg	Val	Val	Cys	Met	Ile	Glu	Trp		
	170					175					180						
cca	gag	cat	ccg	aac	aag	att	tat	gag	aaa	gtg	tac	cac	atc	tgt	gtg	810	
Pro	Glu	His	Pro	Asn	Lys	Ile	Tyr	Glu	Lys	Val	Tyr	His	Ile	Cys	Val		
185					190					195					200		
act	gtg	ctg	atc	tac	ttc	ctc	ccc	ctg	ctg	gtg	att	ggc	tat	gca	tac	858	
Thr	Val	Leu	Ile	Tyr	Phe	Leu	Pro	Leu	Val	Val	Ile	Gly	Tyr	Ala	Tyr		
				205					210					215			
acc	gta	gtg	gga	atc	aca	cta	tgg	gcc	agt	gag	atc	ccc	ggg	gac	tcc	906	
Thr	Val	Val	Gly	Ile	Thr	Leu	Trp	Ala	Ser	Glu	Ile	Pro	Gly	Asp	Ser		
			220					225					230				
tct	gac	cgc	tac	cac	gag	caa	gtc	tct	gcc	aag	cgc	aag	gtg	gtc	aaa	954	
Ser	Asp	Arg	Tyr	His	Glu	Gln	Val	Ser	Ala	Lys	Arg	Lys	Val	Val	Lys		
		235					240					245					
atg	atg	att	gtc	gtg	gtg	tgc	acc	ttc	gcc	atc	tgc	tgg	ctg	ccc	ttc	1002	
Met	Met	Ile	Val	Val	Val	Cys	Thr	Phe	Ala	Ile	Cys	Trp	Leu	Pro	Phe		
		250				255					260						
cac	atc	ttc	ttc	ctc	ctg	ccc	tac	atc	aac	cca	gat	ctc	tac	ctg	aag	1050	
His	Ile	Phe	Phe	Leu	Leu	Pro	Tyr	Ile	Asn	Pro	Asp	Leu	Tyr	Leu	Lys		
265					270					275					280		
aag	ttt	atc	cag	cag	gtc	tac	ctg	gcc	atc	atg	tgg	ctg	gcc	atg	agc	1098	
Lys	Phe	Ile	Gln	Gln	Val	Tyr	Leu	Ala	Ile	Met	Trp	Leu	Ala	Met	Ser		
				285					290					295			
tcc	acc	atg	tac	aac	ccc	atc	atc	tac	tgc	tgc	ctc	aat	gac	agg	ttc	1146	
Ser	Thr	Met	Tyr	Asn	Pro	Ile	Ile	Tyr	Cys	Cys	Leu	Asn	Asp	Arg	Phe		
			300					305					310				
cgt	ctg	ggc	ttc	aag	cat	gcc	ttc	cgg	tgc	tgc	ccc	ttc	atc	agc	gcc	1194	
Arg	Leu	Gly	Phe	Lys	His	Ala	Phe	Arg	Cys	Cys	Pro	Phe	Ile	Ser	Ala		
		315					320					325					
ggc	gac	tat	gag	ggg	ctg	gaa	atg	aaa	tcc	acc	cgg	tat	ctc	cag	acc	1242	
Gly	Asp	Tyr	Glu	Gly	Leu	Glu	Met	Lys	Ser	Thr	Arg	Tyr	Leu	Gln	Thr		
		330				335					340						
cag	ggc	agt	gtg	tac	aaa	gtc	agc	cgc	ctg	gag	acc	acc	atc	tcc	aca	1290	
Gln	Gly	Ser	Val	Tyr	Lys	Val	Ser	Arg	Leu	Glu	Thr	Thr	Ile	Ser	Thr		
345					350					355					360		
gtg	gtg	ggg	gcc	cac	gag	gag	gag	cca	gag	gac	ggc	ccc	aag	gcc	aca	1338	
Val	Val	Gly	Ala	His	Glu	Glu	Glu	Pro	Glu	Asp	Gly	Pro	Lys	Ala	Thr		



Gly Asn Val Val Val Met Trp Ile Ile Leu Ala His Lys Arg Met Arg  
50 55 60

Thr Val Thr Asn Tyr Phe Leu Val Asn Leu Ala Phe Ala Glu Ala Ser  
65 70 75 80

Met Ala Ala Phe Asn Thr Val Val Asn Phe Thr Tyr Ala Val His Asn  
85 90 95

Glu Trp Tyr Tyr Gly Leu Phe Tyr Cys Lys Phe His Asn Phe Xaa Pro  
100 105 110

Ile Ala Ala Val Phe Ala Ser Ile Tyr Ser Met Thr Ala Val Ala Phe  
115 120 125

Asp Arg Tyr Met Ala Ile Ile His Pro Leu Gln Pro Arg Leu Ser Ala  
130 135 140

Thr Ala Thr Lys Val Val Ile Cys Val Xaa Trp Val Leu Ala Leu Leu  
145 150 155 160

Leu Ala Phe Pro Gln Gly Tyr Tyr Ser Thr Thr Glu Thr Met Pro Ser  
165 170 175

Arg Val Val Cys Met Ile Glu Trp Pro Glu His Pro Asn Lys Ile Tyr  
180 185 190

Glu Lys Val Tyr His Ile Cys Val Thr Val Leu Ile Tyr Phe Leu Pro  
195 200 205

Leu Leu Val Ile Gly Tyr Ala Tyr Thr Val Val Gly Ile Thr Leu Trp  
210 215 220

Ala Ser Glu Ile Pro Gly Asp Ser Ser Asp Arg Tyr His Glu Gln Val  
225 230 235 240

Ser Ala Lys Arg Lys Val Val Lys Met Met Ile Val Val Val Cys Thr  
245 250 255

Phe Ala Ile Cys Trp Leu Pro Phe His Ile Phe Phe Leu Leu Pro Tyr  
260 265 270

Ile Asn Pro Asp Leu Tyr Leu Lys Lys Phe Ile Gln Gln Val Tyr Leu

275

280

285

Ala Ile Met Trp Leu Ala Met Ser Ser Thr Met Tyr Asn Pro Ile Ile  
 290 295 300

Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Gly Phe Lys His Ala Phe  
 305 310 315 320

Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu Gly Leu Glu Met  
 325 330 335

Lys Ser Thr Arg Tyr Leu Gln Thr Gln Gly Ser Val Tyr Lys Val Ser  
 340 345 350

Arg Leu Glu Thr Thr Ile Ser Thr Val Val Gly Ala His Glu Glu Glu  
 355 360 365

Pro Glu Asp Gly Pro Lys Ala Thr Pro Xaa Ser Leu Asp Leu Thr Ser  
 370 375 380

Asn Cys Ser Ser Arg Ser Asp Ser Lys Thr Met Thr Glu Ser Phe Ser  
 385 390 395 400

Phe Ser Ser Asn Val Leu Ser  
 405

<210> 293  
 <211> 1826  
 <212> DNA  
 <213> homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1278)..(1278)  
 <223> wherein N is either a "C" or a "T".

<220>  
 <221> misc\_feature  
 <222> (227)..(227)  
 <223> wherein N is either a "T" or a "C".

<220>  
 <221> misc\_feature  
 <222> (536)..(536)  
 <223> wherein N is either a "C" or a "G".

<220>  
 <221> misc\_feature  
 <222> (1498)..(1498)  
 <223> wherein N is either a "G" or an "A".

<400> 293  
 agtctgcact ggagctgcct ggtgaccaga agtttggagt ccgctgacgt cgccgcccag 60  
 atggcctcca ggctgaccct gctgaccctc ctgctgctgc tgctggctgg ggatagagcc 120  
 tcctcaaata caaatgctac cagctccagc tcccaggatc cagagagttt gcaagacaga 180  
 ggcgaaagga aggtcgcaac aacagttatc tccaagatgc tattegntga acccatcctg 240  
 gaggtttcca gcttgccgac aaccaactca acaaccaatt cagccaccaa aataacagct 300  
 aataccactg atgaaccac cacacaaccc accacagagc ccaccaccca acccaccatc 360  
 caaccacccc aaccaactac ccagctccca acagattctc ctaccagacc cactactggg 420  
 tccttctgcc caggacctgt tactctctgc tctgacttgg agagtcattc aacagaggcc 480  
 gtgttggggg atgctttggg agatttctcc ctgaagctct accacgcctt ctcagnaatg 540  
 aagaaggtgg agaccaacat ggctttttcc ccattcagca tcgccagcct ccttaccag 600  
 gtcctgctcg gggctgggca gaacaccaa acaaacctgg agagcatcct ctcttaccac 660  
 aaggacttca cctgtgtcca ccaggccctg aagggttca cgaccaaagg tgtcacctca 720  
 gtctctcaga tcttcacag cccagacctg gccataaggg acacctttgt gaatgcctct 780  
 cggacctgt acagcagcag ccccagagtc ctaagcaaca acagtgcgc caacttgag 840  
 ctcacaca cctgggtggc caagaacacc aacaacaaga tcagccgggt gctagacagt 900  
 ctgccctccg ataccgcct tgcctcctc aatgctatct acctgagtgc caagtgaag 960  
 acaacatttg atcccaagaa aaccagaatg gaacctttc acttcaaaaa ctcagttata 1020  
 aaagtgccca tgatgaatag caagaagtac cctgtggccc atttcattga ccaaactttg 1080  
 aaagccaagg tggggcagct gcagctctcc cacaatctga gtttgggtgat cctggtaccc 1140  
 cagaacctga aacatcgtct tgaagacatg gaacaggctc tcagcccttc tgttttcaag 1200  
 gccatcatgg agaaactgga gatgtccaag ttccagccca ctctcctaac actacccgc 1260  
 atcaaagtga cgaccagnca ggatatgctc tcaatcatgg agaaattgga attcttcgat 1320  
 ttttcttatg accttaacct gtgtgggctg acagaggacc cagatcttca ggtttctgag 1380  
 atgcagcacc agacagtgt ggaactgaca gagactgggg tggaggcggc tgcagcctcc 1440  
 gccatctctg tggcccgcac cctgctggtc tttgaagtgc agcagccctt cctcttontg 1500

ctctggggacc agcagcacaa gttccctgtc ttcattggggc gagtatatga ccccagggcc 1560  
 tgagacctgc aggatcaggt tagggcgagc gctacctctc cagcctcagc tctcagttgc 1620  
 agccctgctg ctgcctgcct ggacttgccc ctgccacctc ctgcctcagg tgtccgctat 1680  
 ccaccaaag ggctcctgag ggtctgggca agggacctgc ttctattagc ctttctccat 1740  
 ggccctgcc tgcctctcaa accacttttt gcagctttct ctagttcaag ttcaccagac 1800  
 tctataaata aaacctgaca gaccat 1826

<210> 294  
 <211> 500  
 <212> PRT  
 <213> homo sapiens

<220>  
 <221> VARIANT  
 <222> (56)..(56)  
 <223> wherein Xaa is either "Val" or "Ala".

<220>  
 <221> VARIANT  
 <222> (159)..(159)  
 <223> wherein Xaa is either "Ala" or "Gly".

<220>  
 <221> VARIANT  
 <222> (480)..(480)  
 <223> wherein Xaa is either "Val" or "Met".

<400> 294

Met	Ala	Ser	Arg	Leu	Thr	Leu	Leu	Thr	Leu	Leu	Leu	Leu	Leu	Ala
1				5				10					15	
Gly	Asp	Arg	Ala	Ser	Ser	Asn	Pro	Asn	Ala	Thr	Ser	Ser	Ser	Gln
			20					25					30	
Asp	Pro	Glu	Ser	Leu	Gln	Asp	Arg	Gly	Glu	Gly	Lys	Val	Ala	Thr
		35					40					45		Thr
Val	Ile	Ser	Lys	Met	Leu	Phe	Xaa	Glu	Pro	Ile	Leu	Glu	Val	Ser
	50					55					60			Ser
Leu	Pro	Thr	Thr	Asn	Ser	Thr	Thr	Asn	Ser	Ala	Thr	Lys	Ile	Thr
65				70					75					80
Asn	Thr	Thr	Asp	Glu	Pro	Thr	Thr	Gln	Pro	Thr	Thr	Glu	Pro	Thr
			85					90					95	Thr

Gln	Pro	Thr	Ile	Gln	Pro	Thr	Gln	Pro	Thr	Thr	Gln	Leu	Pro	Thr	Asp	100	105	110
Ser	Pro	Thr	Gln	Pro	Thr	Thr	Gly	Ser	Phe	Cys	Pro	Gly	Pro	Val	Thr	115	120	125
Leu	Cys	Ser	Asp	Leu	Glu	Ser	His	Ser	Thr	Glu	Ala	Val	Leu	Gly	Asp	130	135	140
Ala	Leu	Val	Asp	Phe	Ser	Leu	Lys	Leu	Tyr	His	Ala	Phe	Ser	Xaa	Met	145	150	155
Lys	Lys	Val	Glu	Thr	Asn	Met	Ala	Phe	Ser	Pro	Phe	Ser	Ile	Ala	Ser	165	170	175
Leu	Leu	Thr	Gln	Val	Leu	Leu	Gly	Ala	Gly	Gln	Asn	Thr	Lys	Thr	Asn	180	185	190
Leu	Glu	Ser	Ile	Leu	Ser	Tyr	Pro	Lys	Asp	Phe	Thr	Cys	Val	His	Gln	195	200	205
Ala	Leu	Lys	Gly	Phe	Thr	Thr	Lys	Gly	Val	Thr	Ser	Val	Ser	Gln	Ile	210	215	220
Phe	His	Ser	Pro	Asp	Leu	Ala	Ile	Arg	Asp	Thr	Phe	Val	Asn	Ala	Ser	225	230	235
Arg	Thr	Leu	Tyr	Ser	Ser	Ser	Pro	Arg	Val	Leu	Ser	Asn	Asn	Ser	Asp	245	250	255
Ala	Asn	Leu	Glu	Leu	Ile	Asn	Thr	Trp	Val	Ala	Lys	Asn	Thr	Asn	Asn	260	265	270
Lys	Ile	Ser	Arg	Leu	Leu	Asp	Ser	Leu	Pro	Ser	Asp	Thr	Arg	Leu	Val	275	280	285
Leu	Leu	Asn	Ala	Ile	Tyr	Leu	Ser	Ala	Lys	Trp	Lys	Thr	Thr	Phe	Asp	290	295	300
Pro	Lys	Lys	Thr	Arg	Met	Glu	Pro	Phe	His	Phe	Lys	Asn	Ser	Val	Ile	305	310	315
Lys	Val	Pro	Met	Met	Asn	Ser	Lys	Lys	Tyr	Pro	Val	Ala	His	Phe	Ile	325	330	335
Asp	Gln	Thr	Leu	Lys	Ala	Lys	Val	Gly	Gln	Leu	Gln	Leu	Ser	His	Asn	340	345	350
Leu	Ser	Leu	Val	Ile	Leu	Val	Pro	Gln	Asn	Leu	Lys	His	Arg	Leu	Glu	355	360	365
Asp	Met	Glu	Gln	Ala	Leu	Ser	Pro	Ser	Val	Phe	Lys	Ala	Ile	Met	Glu	370	375	380
Lys	Leu	Glu	Met	Ser	Lys	Phe	Gln	Pro	Thr	Leu	Leu	Thr	Leu	Pro	Arg	385	390	395
																		400



Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu  
405 410 415

Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu  
420 425 430

Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu  
435 440 445

Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ala Ser Ala Ile Ser Val  
450 455 460

Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Xaa  
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			20					25					30		
Gln	His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Tyr	His	Phe	Ser	Thr	Phe
		35					40					45			
Gln	Cys	Gly	Gly	Ile	Leu	Val	His	Arg	Gln	Trp	Val	Leu	Thr	Ala	Ala
	50					55					60				
His	Cys	Ile	Ser	Asp	Asn	Tyr	Gln	Leu	Trp	Leu	Gly	Arg	His	Asn	Leu
65					70				75					80	
Phe	Asp	Asp	Glu	Asn	Thr	Ala	Gln	Phe	Val	His	Val	Ser	Glu	Ser	Phe
				85					90					95	
Pro	His	Pro	Gly	Phe	Asn	Met	Ser	Leu	Leu	Glu	Asn	His	Thr	Arg	Gln
			100					105					110		
Ala	Asp	Glu	Asp	Tyr	Ser	His	Asp	Leu	Met	Leu	Leu	Arg	Leu	Thr	Glu
		115					120					125			
Pro	Ala	Asp	Thr	Ile	Thr	Asp	Ala	Val	Lys	Val	Val	Glu	Leu	Pro	Thr

130 135 140  
Xaa Glu Pro Glu Val Gly Ser Thr Cys Leu Ala Ser Gly Trp Gly Ser  
145 150 155 160  
Ile Glu Pro Glu Asn Phe Ser Phe Pro Asp Asp Leu Gln Cys Val Asp  
165 170 175  
Leu Lys Ile Leu Pro Asn Asp Glu Cys Xaa Lys Ala His Val Gln Lys  
180 185 190  
Val Thr Asp Phe Met Leu Cys Val Gly His Leu Glu Gly Gly Lys Asp  
195 200 205  
Thr Cys Val Gly Asp Ser Gly Gly Pro Leu Met Cys Asp Gly Val Leu  
210 215 220  
Gln Gly Val Thr Ser Trp Gly Tyr Val Pro Cys Gly Thr Pro Asn Lys  
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 Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile  
 195 200 205  
 Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His  
 210 215 220  
 Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val  
 225 230 235 240  
 Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val  
 245 250 255  
 Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu  
 260 265 270  
 Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp  
 275 280 285  
 Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn  
 290 295 300  
 Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg  
 305 310 315 320  
 Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala  
 325 330 335  
 Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg  
 340 345 350

Asn

<210> 557  
 <211> 1082  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (462)..(462)

<223> wherein N is either a "G" or an "A".

<400> 557

ctgtgcatgg catcatcctg gccccctcta gagctccaat cctccaacca gagccagctc 60  
ttccctcaaa atgctacggc ctgtgacaat gctccagaag cctgggacct gctgcacaga 120  
gtgctgccga catttatcat ctccatctgt ttcttcggcc tcctaggga cctttttgtc 180  
ctgttgggtct tcctcctgcc cggcgggcaa ctgaacgtgg cagaaatcta cctggccaac 240  
ctggcagcct ctgatctggt gtttgtcttg ggcttgcct tctgggcaga gaatatctgg 300  
aaccagttta actggccttt cggagccctc ctctgccgtg tcatcaacgg ggtcatcaag 360  
gccaatttgt tcatcagcat cttcctggtg gtggccatca gccaggaccg ctaccgcgtg 420  
ctggtgcacc ctatggccag cggaaggcag cagcggcgga gacaggcccg ggtcacctgc 480  
gtgctcatct gggttgtggg gggcctcttg agcatcccca cattcctgct gcgatccatc 540  
caagccgtcc cagatctgaa catcaccgcc tgcacctgc tcctcccca tgaggcctgg 600  
cactttgcaa ggattgtgga gttaaattt ctgggtttcc tcctaccact ggctgcatc 660  
gtcttcttca actaccacat cctggcctcc ctgcgaacgc gggaggaggt cagcaggaca 720  
agagtgcggg ggccgaagga tagcaagacc acagcgtga tcctcacgct cgtgggtgcc 780  
ttcctggtct gctgggcccc ttaccacttc tttgccttcc tggaattctt attccaggtg 840  
caagcagtcc gaggtgctt ttgggaggac ttcattgacc tgggcctgca attggccaac 900  
ttctttgct tcactaacag ctccctgaat ccagtaattt atgtctttgt gggccggctc 960  
ttcaggacca aggtctggga actttataaa caatgcacc ctaaaagtct tgctccaata 1020  
tcttcatccc ataggaaaga aatcttccaa cttttctggc ggaattaaaa cagcattgaa 1080  
cc 1082

<210> 558

<211> 353

<212> PRT

<213> Homo sapiens

<400> 558

Met Ala Ser Ser Trp Pro Pro Leu Glu Leu Gln Ser Ser Asn Gln Ser  
1 5 10 15

Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro Glu Ala  
20 25 30

Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser Ile Cys





340

345

350

Asn

<210> 559  
 <211> 1082  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (577)..(577)  
 <223> wherein N is either a "C" or a "G".

<400> 559  
 ctgtgcatgg catcatcctg gccccctcta gagctccaat cctccaacca gagccagctc 60  
 ttccctcaaa atgctacggc ctgtgacaat gctccagaag cctgggacct gctgcacaga 120  
 gtgctgccga catttatcat ctccatctgt ttcttcggcc tcctagggaa cctttttgtc 180  
 ctggttggtct tctcctgcc ccggcgggcaa ctgaacgtgg cagaaatcta cctggccaac 240  
 ctggcagcct ctgatctggt gtttgtcttg ggcttgccct tctgggcaga gaatatctgg 300  
 aaccagttta actggccttt cggagccctc ctctgccgtg tcatcaacgg ggtcatcaag 360  
 gccaatattgt tcatcagcat cttcctggtg gtggccatca gccaggaccg ctaccgcgtg 420  
 ctggtgcacc ctatggccag cggaaggcag cagcggcgga ggcaggcccg ggtcacctgc 480  
 gtgctcatct gggttgtggg gggcctcttg agcatcccca cattcctgct gcgatccatc 540  
 caagccgtcc cagatctgaa catcaccgcc tgcacgtgc tctccccca tgaggcctgg 600  
 cactttgcaa ggattgtgga gttaaattatt ctgggtttcc tcttaccact ggctgcgac 660  
 gtcttcttca actaccacat cctggcctcc ctgcgaacgc gggaggaggt cagcaggaca 720  
 agagtgcggg ggccgaagga tagcaagacc acagcgtga tctcacgct cgtggttgcc 780  
 ttcttggtct gctgggcccc ttaccacttc tttgccttcc tggaattctt attccagggtg 840  
 caagcagtcc gaggtgctt ttgggaggac ttcattgacc tgggcctgca attggccaac 900  
 ttctttgcct tcactaacag ctccctgaat ccagtaattt atgtctttgt gggccggctc 960  
 ttcaggacca aggtctggga actttataaa caatgcaccc ctaaaagtct tgctccaata 1020  
 tcttcatccc ataggaaaga aatcttccaa cttttctggc ggaattaaaa cagcattgaa 1080  
 cc 1082

<210> 560

<211> 353  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> VARIANT  
 <222> (191)..(191)  
 <223> wherein Xaa is either "Leu" or "Val".

<400> 560

Met	Ala	Ser	Ser	Trp	Pro	Pro	Leu	Glu	Leu	Gln	Ser	Ser	Asn	Gln	Ser	1	5	10	15
Gln	Leu	Phe	Pro	Gln	Asn	Ala	Thr	Ala	Cys	Asp	Asn	Ala	Pro	Glu	Ala	20	25	30	
Trp	Asp	Leu	Leu	His	Arg	Val	Leu	Pro	Thr	Phe	Ile	Ile	Ser	Ile	Cys	35	40	45	
Phe	Phe	Gly	Leu	Leu	Gly	Asn	Leu	Phe	Val	Leu	Leu	Val	Phe	Leu	Leu	50	55	60	
Pro	Arg	Arg	Gln	Leu	Asn	Val	Ala	Glu	Ile	Tyr	Leu	Ala	Asn	Leu	Ala	65	70	75	80
Ala	Ser	Asp	Leu	Val	Phe	Val	Leu	Gly	Leu	Pro	Phe	Trp	Ala	Glu	Asn	85	90	95	
Ile	Trp	Asn	Gln	Phe	Asn	Trp	Pro	Phe	Gly	Ala	Leu	Leu	Cys	Arg	Val	100	105	110	
Ile	Asn	Gly	Val	Ile	Lys	Ala	Asn	Leu	Phe	Ile	Ser	Ile	Phe	Leu	Val	115	120	125	
Val	Ala	Ile	Ser	Gln	Asp	Arg	Tyr	Arg	Val	Leu	Val	His	Pro	Met	Ala	130	135	140	
Ser	Gly	Arg	Gln	Gln	Arg	Arg	Arg	Gln	Ala	Arg	Val	Thr	Cys	Val	Leu	145	150	155	160
Ile	Trp	Val	Val	Gly	Gly	Leu	Leu	Ser	Ile	Pro	Thr	Phe	Leu	Leu	Arg	165	170	175	
Ser	Ile	Gln	Ala	Val	Pro	Asp	Leu	Asn	Ile	Thr	Ala	Cys	Ile	Val	Leu	180	185	190	
Leu	Pro	His	Glu	Ala	Trp	His	Phe	Ala	Arg	Ile	Val	Glu	Leu	Asn	Ile	195	200	205	
Leu	Gly	Phe	Leu	Leu	Pro	Leu	Ala	Ala	Ile	Val	Phe	Phe	Asn	Tyr	His	210	215	220	
Ile	Leu	Ala	Ser	Leu	Arg	Thr	Arg	Glu	Glu	Val	Ser	Arg	Thr	Arg	Val	225	230	235	240

Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val  
245 250 255

Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu  
260 265 270

Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp  
275 280 285

Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn  
290 295 300

Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg  
305 310 315 320

Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala  
325 330 335

Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg  
340 345 350

Asn

<210> 561  
<211> 1082  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (705)..(705)  
<223> wherein N is either a "G" or an "A".

<400> 561  
ctgtgcatgg catcatcctg gccccctcta gagctccaat cctccaacca gagccagctc 60  
ttccctcaaa atgctacggc ctgtgacaat gctccagaag cctgggacct gctgcacaga 120  
gtgctgccga catttatcat ctccatctgt ttcttcggcc tcttagggaa cctttttgtc 180  
ctgttggtct tctcctgcc ccggcggcaa ctgaacgtgg cagaaatcta cctggccaac 240  
ctggcagcct ctgatctggt gtttgtcttg ggcttgccct tctgggcaga gaatatctgg 300  
aaccagttta actggccttt cggagccctc ctctgccgtg tcatcaacgg ggtcatcaag 360  
gccaatttgt tcatcagcat cttcctggtg gtggccatca gccaggaccg ctaccgcgtg 420  
ctggtgcacc ctatggccag cggaaggcag cagcggcgga ggcaggcccg ggtcacctgc 480  
gtgctcatct gggttgtggg gggcctcttg agcatcccca cattcctgct gcgatccatc 540  
caagccgtcc cagatctgaa catcacgcc tgcacacctg tctccccca tgaggcctgg 600  
cactttgcaa ggattgtgga gttaaattt ctgggtttcc tctaccact ggctgcgatc 660

gtctttcttca actaccacat cctggcctcc ctgcgaacgc gggaggaggt cagcaggaca 720  
agagtgcggg ggccgaagga tagcaagacc acagcgctga tcctcacgct cgtgggttgcc 780  
ttcctgggtct gctggggcccc ttaccacttc tttgccttcc tggaattctt attccaggtg 840  
caagcagtcc gaggtgctt ttggggaggac ttcattgacc tgggcctgca attggccaac 900  
ttctttgcct tcaactaacag ctccctgaat ccagtaattt atgtctttgt gggccggctc 960  
ttcaggacca aggtctggga actttataaa caatgcaccc ctaaaagtct tgctccaata 1020  
tcttcacccc ataggaaaga aatcttccaa cttttctggc ggaattaaaa cagcattgaa 1080  
cc 1082

<210> 562  
<211> 353  
<212> PRT  
<213> Homo sapiens

<400> 562

Met Ala Ser Ser Trp Pro Pro Leu Glu Leu Gln Ser Ser Asn Gln Ser  
1 5 10 15  
Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro Glu Ala  
20 25 30  
Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser Ile Cys  
35 40 45  
Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe Leu Leu  
50 55 60  
Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala  
65 70 75 80  
Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn  
85 90 95  
Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val  
100 105 110  
Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val  
115 120 125  
Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala  
130 135 140  
Ser Gly Arg Gln Gln Arg Arg Arg Gln Ala Arg Val Thr Cys Val Leu  
145 150 155 160  
Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg  
165 170 175

Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu  
 180 185 190  
 Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile  
 195 200 205  
 Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His  
 210 215 220  
 Ile Leu Ala Ser Leu Arg Thr Arg Lys Glu Val Ser Arg Thr Arg Val  
 225 230 235 240  
 Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val  
 245 250 255  
 Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu  
 260 265 270  
 Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp  
 275 280 285  
 Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn  
 290 295 300  
 Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg  
 305 310 315 320  
 Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala  
 325 330 335  
 Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg  
 340 345 350

Asn

<210> 563  
 <211> 3733  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (40)..(40)  
 <223> wherein N is either a "C" or a "T".

<400> 563  
 atgttctctc cctggaagat atcaatgttt ctgtctgttt gtgaggactc cgtgcccacc 60  
 acggcctctt tcagcgccga catgctcaat gtcaccttgc aagggccac tcttaacggg 120  
 acctttgccc agagcaaagt cccccaagtg gagtggctgg gctgggtcaa caccatccag 180  
 cccccccttc tctgggtgct gttcgtgctg gccaccctag agaacatctt tgtcctcagc 240





aatcatgtaa acatgtgtct tttctgtaga gcataataaa tggatgaggt ttttgcaaaa 3720

aaaaaaaaaaa aaa 3733

<210> 564

<211> 391

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (14)..(14)

<223> wherein Xaa is either "Arg" or "Cys".

<400> 564

Met Phe Ser Pro Trp Lys Ile Ser Met Phe Leu Ser Val Cys Glu Asp  
1 5 10 15

Ser Val Pro Thr Thr Ala Ser Phe Ser Ala Asp Met Leu Asn Val Thr  
20 25 30

Leu Gln Gly Pro Thr Leu Asn Gly Thr Phe Ala Gln Ser Lys Cys Pro  
35 40 45

Gln Val Glu Trp Leu Gly Trp Leu Asn Thr Ile Gln Pro Pro Phe Leu  
50 55 60

Trp Val Leu Phe Val Leu Ala Thr Leu Glu Asn Ile Phe Val Leu Ser  
65 70 75 80

Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu  
85 90 95

Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe  
100 105 110

Trp Ala Ile Thr Ile Ser Asn Asn Phe Asp Trp Leu Phe Gly Glu Thr  
115 120 125

Leu Cys Arg Val Val Asn Ala Ile Ile Ser Met Asn Leu Tyr Ser Ser  
130 135 140

Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg Tyr Leu Ala Leu Val  
145 150 155 160

Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys Leu  
165 170 175

Tyr Ser Leu Val Ile Trp Gly Cys Thr Leu Leu Leu Ser Ser Pro Met  
180 185 190

Leu Val Phe Arg Thr Met Lys Glu Tyr Ser Asp Glu Gly His Asn Val  
195 200 205



Thr Ala Cys Val Ile Ser Tyr Pro Ser Leu Ile Trp Glu Val Phe Thr  
 210 215 220  
 Asn Met Leu Leu Asn Val Val Gly Phe Leu Leu Pro Leu Ser Val Ile  
 225 230 235 240  
 Thr Phe Cys Thr Met Gln Ile Met Gln Val Leu Arg Asn Asn Glu Met  
 245 250 255  
 Gln Lys Phe Lys Glu Ile Gln Thr Glu Arg Arg Ala Thr Val Leu Val  
 260 265 270  
 Leu Val Val Leu Leu Leu Phe Ile Ile Cys Trp Leu Pro Phe Gln Ile  
 275 280 285  
 Ser Thr Phe Leu Asp Thr Leu His Arg Leu Gly Ile Leu Ser Ser Cys  
 290 295 300  
 Gln Asp Glu Arg Ile Ile Asp Val Ile Thr Gln Ile Ala Ser Phe Met  
 305 310 315 320  
 Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val Tyr Val Ile Val Gly  
 325 330 335  
 Lys Arg Phe Arg Lys Lys Ser Trp Glu Val Tyr Gln Gly Val Cys Gln  
 340 345 350  
 Lys Gly Gly Cys Arg Ser Glu Pro Ile Gln Met Glu Asn Ser Met Gly  
 355 360 365  
 Thr Leu Arg Thr Ser Ile Ser Val Glu Arg Gln Ile His Lys Leu Gln  
 370 375 380  
 Asp Trp Ala Gly Ser Arg Gln  
 385 390

<210> 565  
 <211> 3733  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (933)..(933)  
 <223> wherein N is either a "T" or a "C".

<400> 565  
 atgttctctc cctggaagat atcaatgttt ctgtctgttc gtgaggactc cgtgcccacc 60  
 acggcctctt tcagcgccga catgctcaat gtcaccttgc aagggccac tcttaacggg 120  
 acctttgccc agagcaaagtg cccccaagtg gagtggctgg gctgggtcaa caccatccag 180  
 ccccccttcc tctgggtgct gttcgtgctg gccaccctag agaacatctt tgtcctcagc 240  
 gtcttctgcc tgcacaagag cagctgcacg gtggcagaga tctacctggg gaacctggcc 300



ccaataacta	ttgcacaacc	acctgtccct	gcctcagttc	ccttttatgt	aacatgaagt	2040
cgttgtgagg	gttaaaggca	gtaacaggta	taaagtactt	agaaaagcaa	agggtgctac	2100
gtacatgtga	ggcatcatta	cgcagacgta	actgggatat	gtttactata	aggaaaagac	2160
actgaggtct	agaaatagct	ccgtggagca	gaatcagtat	tgggagccgg	tggcgggtgtg	2220
aagcaccagt	gtctggcaca	cagtaggtgc	tcattggctc	ccttccacct	gtcattccca	2280
ccaccctgag	gccccaacg	ccacacacac	aggagcattt	ggagagaagg	ccatgtcttc	2340
aaagtctgat	ttgtgatgag	gcagaggaag	atatttctaa	tcggtcttgc	ccagaggatc	2400
acagtgctga	gacccccac	caccagccgg	tacctgggaa	gggggagagt	gcaggcctgc	2460
tcagggactg	ttcctgtctc	agcaaccaag	ggattgttcc	tgtcaatcaa	tggtttattg	2520
gaaggtggcc	cagtatgagc	cctagaagag	tgtgaaaagg	aatggcaatg	gtgttcacca	2580
tcggcagtg	cagggcagca	ctcattcact	tgataaatga	atatttatta	gctggttgga	2640
gagctagaac	ctggagagct	agaacctgga	gaactagaac	ctggagggct	agaacctgga	2700
gaggctagaa	ccaagaaggg	ctagaacctg	gaggggctag	aacctagaga	agctaaaacc	2760
tgagctagaa	gctggaggac	tagaacctgg	agggctggaa	tctgaagggc	tagaacctgg	2820
agggctggaa	tctggagagc	tagaacctgg	agggctagaa	cctggagggc	tagaacctag	2880
aagggctaga	acctggaggg	ctggaatctg	gagagctaga	acctggaggg	ctagaacctg	2940
gagggctaga	acctagaagg	gctagaacct	ggagggctag	aacctggcag	gttagaacct	3000
agaagggcta	gaacctggag	agccagaacc	tggagggcta	gaacctggaa	gggctagaac	3060
ctgtagagct	agaacatgga	gagctagaac	ccggcaggct	agaacctggc	aagctagaac	3120
ctggagggaa	tgaacctgga	gggctagaac	ctggagaatg	agaaaaattt	acatggcaaa	3180
gagcccataa	atcctgacca	atccaactct	gaattttaaa	gcaaaagcgt	gaaaaaaaaag	3240
attccctcct	tacccccaac	ccactctttt	ttcccaccac	ccactctcct	ctgcctcagt	3300
aagtatctgg	aggaagaaaa	caggtgaaag	aagaagtaaa	aaccatttag	tattagtatt	3360
agaatgaagt	caaactgtgc	cacacatggt	gaatgaaaaa	aaaaaaaaag	aggctgtggt	3420
ttgtcacaca	gggcagtcac	tcagcaccag	agcacgtgat	ggtctgagac	tctcttagga	3480
gcagagctct	gccgcaatgg	ccatgtgggg	atccacacct	ggtctgaggg	gcaactgagt	3540
ctgcgggaga	agagcggccc	tatgcatggt	gtagatgcc	tgataaagaa	catctgtcct	3600
gtgaaagact	caatgagctg	ttatgttgta	aacaggaagc	atttcacatc	caaacgagaa	3660
aatcatgtaa	acatgtgtct	tttctgtaga	gcataataaa	tggatgaggt	ttttgcaaaa	3720

aaaaaaaaaa aaa

3733

<210> 566  
<211> 391  
<212> PRT  
<213> Homo sapiens

<400> 566

Met Phe Ser Pro Trp Lys Ile Ser Met Phe Leu Ser Val Arg Glu Asp  
1 5 10 15  
Ser Val Pro Thr Thr Ala Ser Phe Ser Ala Asp Met Leu Asn Val Thr  
20 25 30  
Leu Gln Gly Pro Thr Leu Asn Gly Thr Phe Ala Gln Ser Lys Cys Pro  
35 40 45  
Gln Val Glu Trp Leu Gly Trp Leu Asn Thr Ile Gln Pro Pro Phe Leu  
50 55 60  
Trp Val Leu Phe Val Leu Ala Thr Leu Glu Asn Ile Phe Val Leu Ser  
65 70 75 80  
Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu  
85 90 95  
Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe  
100 105 110  
Trp Ala Ile Thr Ile Ser Asn Asn Phe Asp Trp Leu Phe Gly Glu Thr  
115 120 125  
Leu Cys Arg Val Val Asn Ala Ile Ile Ser Met Asn Leu Tyr Ser Ser  
130 135 140  
Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg Tyr Leu Ala Leu Val  
145 150 155 160  
Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys Leu  
165 170 175  
Tyr Ser Leu Val Ile Trp Gly Cys Thr Leu Leu Leu Ser Ser Pro Met  
180 185 190  
Leu Val Phe Arg Thr Met Lys Glu Tyr Ser Asp Glu Gly His Asn Val  
195 200 205  
Thr Ala Cys Val Ile Ser Tyr Pro Ser Leu Ile Trp Glu Val Phe Thr  
210 215 220  
Asn Met Leu Leu Asn Val Val Gly Phe Leu Leu Pro Leu Ser Val Ile  
225 230 235 240  
Thr Phe Cys Thr Met Gln Ile Met Gln Val Leu Arg Asn Asn Glu Met

245	250	255
Gln Lys Phe Lys Glu Ile Gln Thr Glu Arg Arg Ala Thr Val Leu Val		
260	265	270
Leu Val Val Leu Leu Leu Phe Ile Ile Cys Trp Leu Pro Phe Gln Ile		
275	280	285
Ser Thr Phe Leu Asp Thr Leu His Arg Leu Gly Ile Leu Ser Ser Cys		
290	295	300
Gln Asp Glu Arg Ile Ile Asp Val Ile Thr Gln Ile Ala Ser Phe Met		
305	310	315
Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val Tyr Val Ile Val Gly		
325	330	335
Lys Arg Phe Arg Lys Lys Ser Trp Glu Val Tyr Gln Gly Val Cys Gln		
340	345	350
Lys Gly Gly Cys Arg Ser Glu Pro Ile Gln Met Glu Asn Ser Met Gly		
355	360	365
Thr Leu Arg Thr Ser Ile Ser Val Glu Arg Gln Ile His Lys Leu Gln		
370	375	380
Asp Trp Ala Gly Ser Arg Gln		
385	390	

<210> 567  
 <211> 3733  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> misc\_feature  
 <222> (1061)..(1061)  
 <223> wherein N is either a "G" or an "A".

<400> 567	
atgttctctc cctggaagat atcaatgttt ctgtctgttc gtgaggactc cgtgcccacc	60
acggcctctt tcagcgccga catgctcaat gtcaccttgc aagggccac tcttaacggg	120
acctttgccc agagcaaagtg cccccaagtg gagggtgtgg gctgggtcaa caccatccag	180
cccccttcc tctgggtgct gttcgtgctg gccaccctag agaacatctt tgtcctcagc	240
gtcttctgcc tgcacaagag cagctgcacg gtggcagaga tctacctggg gaacctggcc	300
gcagcagacc tgatcctggc ctgctgggtg cccttctggg ccatcaccat ctccaacaac	360
ttcgactggc tctttgggga gacgctctgc cgcgtggtga atgccattat ctccatgaac	420
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<210> 568  
 <211> 391  
 <212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (354)..(354)

<223> wherein Xaa is either "Gly" or "Glu".

<400> 568

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			20					25					30			
Leu	Gln	Gly	Pro	Thr	Leu	Asn	Gly	Thr	Phe	Ala	Gln	Ser	Lys	Cys	Pro	
		35					40					45				
Gln	Val	Glu	Trp	Leu	Gly	Trp	Leu	Asn	Thr	Ile	Gln	Pro	Pro	Phe	Leu	
		50				55					60					
Trp	Val	Leu	Phe	Val	Leu	Ala	Thr	Leu	Glu	Asn	Ile	Phe	Val	Leu	Ser	
65					70					75					80	
Val	Phe	Cys	Leu	His	Lys	Ser	Ser	Cys	Thr	Val	Ala	Glu	Ile	Tyr	Leu	
				85					90					95		
Gly	Asn	Leu	Ala	Ala	Ala	Asp	Leu	Ile	Leu	Ala	Cys	Gly	Leu	Pro	Phe	
			100					105					110			
Trp	Ala	Ile	Thr	Ile	Ser	Asn	Asn	Phe	Asp	Trp	Leu	Phe	Gly	Glu	Thr	
			115				120					125				
Leu	Cys	Arg	Val	Val	Asn	Ala	Ile	Ile	Ser	Met	Asn	Leu	Tyr	Ser	Ser	
			130			135					140					
Ile	Cys	Phe	Leu	Met	Leu	Val	Ser	Ile	Asp	Arg	Tyr	Leu	Ala	Leu	Val	
145					150					155					160	
Lys	Thr	Met	Ser	Met	Gly	Arg	Met	Arg	Gly	Val	Arg	Trp	Ala	Lys	Leu	
				165					170					175		
Tyr	Ser	Leu	Val	Ile	Trp	Gly	Cys	Thr	Leu	Leu	Leu	Ser	Ser	Pro	Met	
			180					185					190			
Leu	Val	Phe	Arg	Thr	Met	Lys	Glu	Tyr	Ser	Asp	Glu	Gly	His	Asn	Val	
			195				200					205				
Thr	Ala	Cys	Val	Ile	Ser	Tyr	Pro	Ser	Leu	Ile	Trp	Glu	Val	Phe	Thr	
			210			215					220					
Asn	Met	Leu	Leu	Asn	Val	Val	Gly	Phe	Leu	Leu	Pro	Leu	Ser	Val	Ile	
225				230						235					240	
Thr	Phe	Cys	Thr	Met	Gln	Ile	Met	Gln	Val	Leu	Arg	Asn	Asn	Glu	Met	
				245					250					255		



Gln Lys Phe Lys Glu Ile Gln Thr Glu Arg Arg Ala Thr Val Leu Val  
 260 265 270  
 Leu Val Val Leu Leu Leu Phe Ile Ile Cys Trp Leu Pro Phe Gln Ile  
 275 280 285  
 Ser Thr Phe Leu Asp Thr Leu His Arg Leu Gly Ile Leu Ser Ser Cys  
 290 295 300  
 Gln Asp Glu Arg Ile Ile Asp Val Ile Thr Gln Ile Ala Ser Phe Met  
 305 310 315 320  
 Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val Tyr Val Ile Val Gly  
 325 330 335  
 Lys Arg Phe Arg Lys Lys Ser Trp Glu Val Tyr Gln Gly Val Cys Gln  
 340 345 350  
 Lys Glu Gly Cys Arg Ser Glu Pro Ile Gln Met Glu Asn Ser Met Gly  
 355 360 365  
 Thr Leu Arg Thr Ser Ile Ser Val Glu Arg Gln Ile His Lys Leu Gln  
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 Asp Trp Ala Gly Ser Arg Gln  
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<210> 569  
 <211> 3405  
 <212> DNA  
 <213> Homo sapiens

<400> 569  
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 gctccttctc agccttggtg ctgtaactgc tgctcagtcc accattgagg aacaggccaa 180  
 gacatttttg gacaagttta accacgaagc cgaagacctg ttctatcaaa gttcacttgc 240  
 ttcttggaat tataacacca atattactga agagaatgtc caaaacatga ataatgctgg 300  
 ggacaaatgg tctgcctttt taaaggaaca gtccacactt gcccaaagt atccactaca 360  
 agaaattcag aatctcacag tcaagttca gctgcaggct cttcagcaaa atgggtcttc 420  
 agtgctctca gaagacaaga gcaaacgggt gaacacaatt ctaaatacaa tgagcaccat 480  
 ctacagtact ggaaaagttt gtaaccaga taatccacaa gaatgcttat tacttgaacc 540  
 aggtttgaat gaaataatgg caaacagttt agactacaat gagaggctct gggcttgga 600  
 aagctggaga tctgaggtcg gcaagcagct gaggccatta tatgaagagt atgtggtctt 660  
 gaaaaatgag atggcaagag caaatcatta tgaggactat ggggattatt ggagaggaga 720





Gln	Met	Tyr	Pro	Leu	Gln	Glu	Ile	Gln	Asn	Leu	Thr	Val	Lys	Leu	Gln	
				85					90					95		
Leu	Gln	Ala	Leu	Gln	Gln	Asn	Gly	Ser	Ser	Val	Leu	Ser	Glu	Asp	Lys	
			100					105					110			
Ser	Lys	Arg	Leu	Asn	Thr	Ile	Leu	Asn	Thr	Met	Ser	Thr	Ile	Tyr	Ser	
			115				120					125				
Thr	Gly	Lys	Val	Cys	Asn	Pro	Asp	Asn	Pro	Gln	Glu	Cys	Leu	Leu	Leu	
	130					135					140					
Glu	Pro	Gly	Leu	Asn	Glu	Ile	Met	Ala	Asn	Ser	Leu	Asp	Tyr	Asn	Glu	
145					150					155					160	
Arg	Leu	Trp	Ala	Trp	Glu	Ser	Trp	Arg	Ser	Glu	Val	Gly	Lys	Gln	Leu	
				165					170					175		
Arg	Pro	Leu	Tyr	Glu	Glu	Tyr	Val	Val	Leu	Lys	Asn	Glu	Met	Ala	Arg	
			180					185					190			
Ala	Asn	His	Tyr	Glu	Asp	Tyr	Gly	Asp	Tyr	Trp	Arg	Gly	Asp	Tyr	Glu	
		195					200					205				
Val	Asn	Gly	Val	Asp	Gly	Tyr	Asp	Tyr	Ser	Arg	Gly	Gln	Leu	Ile	Glu	
	210					215					220					
Asp	Val	Glu	His	Thr	Phe	Glu	Glu	Ile	Lys	Pro	Leu	Tyr	Glu	His	Leu	
225					230					235					240	
His	Ala	Tyr	Val	Arg	Ala	Lys	Leu	Met	Asn	Ala	Tyr	Pro	Ser	Tyr	Ile	
				245					250					255		
Ser	Pro	Ile	Gly	Cys	Leu	Pro	Ala	His	Leu	Leu	Gly	Asp	Met	Trp	Gly	
			260					265					270			
Arg	Phe	Trp	Thr	Asn	Leu	Tyr	Ser	Leu	Thr	Val	Pro	Phe	Gly	Gln	Lys	
			275				280					285				
Pro	Asn	Ile	Asp	Val	Thr	Asp	Ala	Met	Val	Asp	Gln	Ala	Trp	Asp	Ala	
	290					295					300					
Gln	Arg	Ile	Phe	Lys	Glu	Ala	Glu	Lys	Phe	Phe	Val	Ser	Val	Gly	Leu	
305					310					315					320	
Pro	Asn	Met	Thr	Gln	Gly	Phe	Trp	Glu	Asn	Ser	Met	Leu	Thr	Asp	Pro	
				325					330					335		
Gly	Asn	Val	Gln	Lys	Ala	Val	Cys	His	Pro	Thr	Ala	Trp	Asp	Leu	Gly	
			340					345					350			
Lys	Gly	Asp	Phe	Arg	Ile	Leu	Met	Cys	Thr	Lys	Val	Thr	Met	Asp	Asp	
		355					360						365			
Phe	Leu	Thr	Ala	His	His	Glu	Met	Gly	His	Ile	Gln	Tyr	Asp	Met	Ala	
	370					375					380					

Tyr	Ala	Ala	Gln	Pro	Phe	Leu	Leu	Arg	Asn	Gly	Ala	Asn	Glu	Gly	Phe	385	390	395	400
His	Glu	Ala	Val	Gly	Glu	Ile	Met	Ser	Leu	Ser	Ala	Ala	Thr	Pro	Lys	405	410	415	
His	Leu	Lys	Ser	Ile	Gly	Leu	Leu	Ser	Pro	Asp	Phe	Gln	Glu	Asp	Asn	420	425	430	
Glu	Thr	Glu	Ile	Asn	Phe	Leu	Leu	Lys	Gln	Ala	Leu	Thr	Ile	Val	Gly	435	440	445	
Thr	Leu	Pro	Phe	Thr	Tyr	Met	Leu	Glu	Lys	Trp	Arg	Trp	Met	Val	Phe	450	455	460	
Lys	Gly	Glu	Ile	Pro	Lys	Asp	Gln	Trp	Met	Lys	Lys	Trp	Trp	Glu	Met	465	470	475	480
Lys	Arg	Glu	Ile	Val	Gly	Val	Val	Glu	Pro	Val	Pro	His	Asp	Glu	Thr	485	490	495	
Tyr	Cys	Asp	Pro	Ala	Ser	Leu	Phe	His	Val	Ser	Asn	Asp	Tyr	Ser	Phe	500	505	510	
Ile	Arg	Tyr	Tyr	Thr	Arg	Thr	Leu	Tyr	Gln	Phe	Gln	Phe	Gln	Glu	Ala	515	520	525	
Leu	Cys	Gln	Ala	Ala	Lys	His	Glu	Gly	Pro	Leu	His	Lys	Cys	Asp	Ile	530	535	540	
Ser	Asn	Ser	Thr	Glu	Ala	Gly	Gln	Lys	Leu	Phe	Asn	Met	Leu	Arg	Leu	545	550	555	560
Gly	Lys	Ser	Glu	Pro	Trp	Thr	Leu	Ala	Leu	Glu	Asn	Val	Val	Gly	Ala	565	570	575	
Lys	Asn	Met	Asn	Val	Arg	Pro	Leu	Leu	Asn	Tyr	Phe	Glu	Pro	Leu	Phe	580	585	590	
Thr	Trp	Leu	Lys	Asp	Gln	Asn	Lys	Asn	Ser	Phe	Val	Gly	Trp	Ser	Thr	595	600	605	
Asp	Trp	Ser	Pro	Tyr	Ala	Asp	Gln	Ser	Ile	Lys	Val	Arg	Ile	Ser	Leu	610	615	620	
Lys	Ser	Ala	Leu	Gly	Asp	Lys	Ala	Tyr	Glu	Trp	Asn	Asp	Asn	Glu	Met	625	630	635	640
Tyr	Leu	Phe	Arg	Ser	Ser	Val	Ala	Tyr	Ala	Met	Arg	Gln	Tyr	Phe	Leu	645	650	655	
Lys	Val	Lys	Asn	Gln	Met	Ile	Leu	Phe	Gly	Glu	Glu	Asp	Val	Arg	Val	660	665	670	
Ala	Asn	Leu	Lys	Pro	Arg	Ile	Ser	Phe	Asn	Phe	Phe	Val	Thr	Ala	Pro	675	680	685	

Lys Asn Val Ser Asp Ile Ile Pro Arg Thr Glu Val Glu Lys Ala Ile  
690 695 700

Arg Met Ser Arg Ser Arg Ile Asn Asp Ala Phe Arg Leu Asn Asp Asn  
705 710 715 720

Ser Leu Glu Phe Leu Gly Ile Gln Pro Thr Leu Gly Pro Pro Asn Gln  
725 730 735

Pro Pro Val Ser Ile Trp Leu Ile Val Phe Gly Val Val Met Gly Val  
740 745 750

Ile Val Val Gly Ile Val Ile Leu Ile Phe Thr Gly Ile Arg Asp Arg  
755 760 765

Lys Lys Lys Asn Lys Ala Arg Ser Gly Glu Asn Pro Tyr Ala Ser Ile  
770 775 780

Asp Ile Ser Lys Gly Glu Asn Asn Pro Gly Phe Gln Asn Thr Asp Asp  
785 790 795 800

Val Gln Thr Ser Phe  
805

<210> 571  
<211> 1284  
<212> DNA  
<213> Homo sapiens

<400> 571  
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 gtcgtcgacc ccacgaaacc atag 1284

<210> 572  
 <211> 427  
 <212> PRT  
 <213> Homo sapiens

<400> 572

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 Leu Ser His Gly Gln Leu His Val Glu His Asp Gly Glu Ser Cys Ser  
 20 25 30  
 Asn Ser Ser His Gln Gln Ile Leu Glu Thr Gly Glu Gly Ser Pro Ser  
 35 40 45  
 Leu Lys Ile Ala Pro Ala Asn Ala Asp Phe Ala Phe Arg Phe Tyr Tyr  
 50 55 60  
 Leu Ile Ala Ser Glu Thr Pro Gly Lys Asn Ile Phe Phe Ser Pro Leu  
 65 70 75 80  
 Ser Ile Ser Ala Ala Tyr Ala Met Leu Ser Leu Gly Ala Cys Ser His  
 85 90 95  
 Ser Arg Ser Gln Ile Leu Glu Gly Leu Gly Phe Asn Leu Thr Glu Leu  
 100 105 110  
 Ser Glu Ser Asp Val His Arg Gly Phe Gln His Leu Leu His Thr Leu  
 115 120 125  
 Asn Leu Pro Gly His Gly Leu Glu Thr Arg Val Gly Ser Ala Leu Phe  
 130 135 140  
 Leu Ser His Asn Leu Lys Phe Leu Ala Lys Phe Leu Asn Asp Thr Met  
 145 150 155 160  
 Ala Val Tyr Glu Ala Lys Leu Phe His Thr Asn Phe Tyr Asp Thr Val  
 165 170 175





<223> wherein N is either a "C" or a "T".

<400> 573

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gagacagggtg agggctcccc cagcctcaag atagcccctg ccaatgctga ctttgccttc 180
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ttccagcacc tctgcacac tctcaacctc ccgggccatg ggctggaaac acgcgtgggc 420
agtgtctgtg tctgagcca caacctgaag ttccttgcaa aattcctgaa tgacaccatg 480
gccgtctatg aggctaaact cttccacacc aacttctacg acactgtggg cacaatccag 540
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ctcaagaagg acgtcttgat ggtgctgggtg aattacattt acttcaaagc cctgtgggag 660
aaaccattca tttcctcaag gaccactccc aaagactttt atgttgatga gaacacaaca 720
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gtcgtcgacc ccacgaaacc atag 1284
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<210> 574

<211> 427

<212> PRT

<213> Homo sapiens

<400> 574

Met His Leu Ile Asp Tyr Leu Leu Leu Leu Leu Val Gly Leu Leu Ala

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Leu Ser His Gly	Gln Leu His Val	Glu His Asp Gly	Glu Ser Cys Ser
20	25	30	
Asn Ser Ser His	Gln Gln Ile Leu	Glu Thr Gly Glu	Gly Ser Pro Ser
35	40	45	
Leu Lys Ile Ala	Pro Ala Asn Ala	Asp Phe Ala Phe	Arg Phe Tyr Tyr
50	55	60	
Leu Ile Ala Ser	Glu Thr Pro Gly	Lys Asn Ile Phe	Phe Ser Pro Leu
65	70	75	80
Ser Ile Ser Ala	Ala Tyr Ala Met	Leu Ser Leu Gly	Ala Cys Ser His
85	90	95	
Ser Arg Ser Gln	Ile Leu Glu Gly	Leu Gly Phe Asn	Leu Thr Glu Leu
100	105	110	
Ser Glu Ser Asp	Val His Arg Gly	Phe Gln His Leu	Leu His Thr Leu
115	120	125	
Asn Leu Pro Gly	His Gly Leu Glu	Thr Arg Val Gly	Ser Ala Leu Phe
130	135	140	
Leu Ser His Asn	Leu Lys Phe Leu	Ala Lys Phe Leu	Asn Asp Thr Met
145	150	155	160
Ala Val Tyr Glu	Ala Lys Leu Phe	His Thr Asn Phe	Tyr Asp Thr Val
165	170	175	
Gly Thr Ile Gln	Leu Ile Asn Asp	His Val Lys Lys	Glu Thr Arg Gly
180	185	190	
Lys Ile Val Asp	Leu Val Ser Glu	Leu Lys Lys Asp	Val Leu Met Val
195	200	205	
Leu Val Asn Tyr	Ile Tyr Phe Lys	Ala Leu Trp Glu	Lys Pro Phe Ile
210	215	220	
Ser Ser Arg Thr	Thr Pro Lys Asp	Phe Tyr Val Asp	Glu Asn Thr Thr
225	230	235	240
Val Arg Val Pro	Met Met Leu Gln	Asp Gln Glu His	His Trp Tyr Leu
245	250	255	
His Asp Arg Tyr	Leu Pro Cys Ser	Val Leu Arg Met	Asp Tyr Lys Gly
260	265	270	
Asp Ala Thr Val	Phe Phe Ile Leu	Pro Asn Gln Gly	Lys Met Arg Glu
275	280	285	
Ile Glu Glu Val	Leu Thr Pro Glu	Met Leu Met Arg	Trp Asn Asn Leu
290	295	300	
Leu Arg Lys Arg	Asn Phe Tyr Lys	Lys Leu Glu Leu	His Leu Pro Lys

305		310		315		320
Phe Ser Ile Ser Gly Ser Tyr Val Leu Asp Gln Ile Leu Pro Arg Leu						
	325			330		335
Gly Phe Thr Asp Leu Phe Ser Lys Trp Ala Asp Leu Ser Gly Ile Thr						
	340			345		350
Lys Gln Gln Lys Leu Glu Ala Ser Lys Ser Phe His Lys Ala Thr Leu						
	355			360		365
Asp Val Asp Glu Ala Gly Thr Glu Ala Ala Ala Ala Thr Thr Phe Ala						
	370			375		380
Ile Lys Phe Phe Ser Ala Gln Thr Asn Arg His Ile Leu Arg Phe Asn						
	385			390		395
Arg Pro Phe Leu Val Val Ile Phe Ser Thr Ser Thr Gln Ser Val Leu						
	405			410		415
Phe Leu Gly Lys Val Val Asp Pro Thr Lys Pro						
	420			425		

<210> 575  
 <211> 1284  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (597)..(597)  
 <223> wherein N is either a "T" or a "C".

<400> 575  
 atgcatctta tcgactacct gctcctcctg ctggttgac tactggccct ttctcatggc 60  
 cagctgcacg ttgagcatga tgggtgagagt tgcagtaaca gctccaccca gcagattctg 120  
 gagacaggtg agggctcccc cagcctcaag atagcccctg ccaatgctga ctttgccttc 180  
 cgcttctact acctgatcgc ttcgagagacc ccggggaaga acatcttttt ctccccgctg 240  
 agcatctcgg cggcctaagc catgctttcc ctgggggcct gctcacacag ccgcagccag 300  
 atccttgagg gcttgggctt caacctcacc gagctgtctg agtccgatgt ccataggggc 360  
 ttccagcacc tctgcacac tctcaacctc cccggccatg ggctggaaac acgcgtgggc 420  
 agtgctctgt tctgagcca caacctgaag ttccttgcaa aattcctgaa tgacaccatg 480  
 gccgtctatg aggctaaact cttccacacc aacttctacg aactgtggg cacaatccag 540  
 cttatcaacg accacgtcaa gaaggaaact cgagggaaga ttgtggattt ggtcagcgag 600  
 ctcaagaagg acgtcttgat ggtgctgggtg aattacattt acttcaaagc cctgtgggag 660

aaaccattca tttcctcaag gaccactccc aaagacttct atgttgatga gaacacaaca 720  
 gtccgggtgc ccatgatgct gcaggaccag gagcatcact ggtatcttca tgacagatac 780  
 ttgccctgct cgggtgctacg gatggattac aaaggagacg caaccgtgtt tttcattctc 840  
 cctaaccaag gcaaaatgag ggagattgaa gaggttctga ctccagagat gctaatagagg 900  
 tggaacaact tgttgcgga gaggaatttt tacaagaagc tagagttgca tcttccaag 960  
 ttctccattt ctggctccta tgtattagat cagattttgc ccaggctggg cttcacggat 1020  
 ctgttctcca agtgggctga cttatccggc atcaccaaac agcaaaaact ggaggcatcc 1080  
 aaaagtttcc acaaggccac cttggacgtg gatgaggctg gcaccgaggc tgcagcagcc 1140  
 accacgttcg cgatcaaatt cttctctgcc cagaccaatc gccacatcct gcgattcaac 1200  
 cgcccttcc ttgtggtgat cttttccacc agcaccacaga gtgtcctctt tctgggcaag 1260  
 gtcgtcgacc ccacgaaacc atag 1284

<210> 576  
 <211> 427  
 <212> PRT  
 <213> Homo sapiens  
 <400> 576

Met His Leu Ile Asp Tyr Leu Leu Leu Leu Leu Val Gly Leu Leu Ala  
 1 5 10 15  
 Leu Ser His Gly Gln Leu His Val Glu His Asp Gly Glu Ser Cys Ser  
 20 25 30  
 Asn Ser Ser His Gln Gln Ile Leu Glu Thr Gly Glu Gly Ser Pro Ser  
 35 40 45  
 Leu Lys Ile Ala Pro Ala Asn Ala Asp Phe Ala Phe Arg Phe Tyr Tyr  
 50 55 60  
 Leu Ile Ala Ser Glu Thr Pro Gly Lys Asn Ile Phe Phe Ser Pro Leu  
 65 70 75 80  
 Ser Ile Ser Ala Ala Tyr Ala Met Leu Ser Leu Gly Ala Cys Ser His  
 85 90 95  
 Ser Arg Ser Gln Ile Leu Glu Gly Leu Gly Phe Asn Leu Thr Glu Leu  
 100 105 110  
 Ser Glu Ser Asp Val His Arg Gly Phe Gln His Leu Leu His Thr Leu  
 115 120 125  
 Asn Leu Pro Gly His Gly Leu Glu Thr Arg Val Gly Ser Ala Leu Phe  
 130 135 140

Leu	Ser	His	Asn	Leu	Lys	Phe	Leu	Ala	Lys	Phe	Leu	Asn	Asp	Thr	Met	145	150	155	160
Ala	Val	Tyr	Glu	Ala	Lys	Leu	Phe	His	Thr	Asn	Phe	Tyr	Asp	Thr	Val	165	170	175	
Gly	Thr	Ile	Gln	Leu	Ile	Asn	Asp	His	Val	Lys	Lys	Glu	Thr	Arg	Gly	180	185	190	
Lys	Ile	Val	Asp	Leu	Val	Ser	Glu	Leu	Lys	Lys	Asp	Val	Leu	Met	Val	195	200	205	
Leu	Val	Asn	Tyr	Ile	Tyr	Phe	Lys	Ala	Leu	Trp	Glu	Lys	Pro	Phe	Ile	210	215	220	
Ser	Ser	Arg	Thr	Thr	Pro	Lys	Asp	Phe	Tyr	Val	Asp	Glu	Asn	Thr	Thr	225	230	235	240
Val	Arg	Val	Pro	Met	Met	Leu	Gln	Asp	Gln	Glu	His	His	Trp	Tyr	Leu	245	250	255	
His	Asp	Arg	Tyr	Leu	Pro	Cys	Ser	Val	Leu	Arg	Met	Asp	Tyr	Lys	Gly	260	265	270	
Asp	Ala	Thr	Val	Phe	Phe	Ile	Leu	Pro	Asn	Gln	Gly	Lys	Met	Arg	Glu	275	280	285	
Ile	Glu	Glu	Val	Leu	Thr	Pro	Glu	Met	Leu	Met	Arg	Trp	Asn	Asn	Leu	290	295	300	
Leu	Arg	Lys	Arg	Asn	Phe	Tyr	Lys	Lys	Leu	Glu	Leu	His	Leu	Pro	Lys	305	310	315	320
Phe	Ser	Ile	Ser	Gly	Ser	Tyr	Val	Leu	Asp	Gln	Ile	Leu	Pro	Arg	Leu	325	330	335	
Gly	Phe	Thr	Asp	Leu	Phe	Ser	Lys	Trp	Ala	Asp	Leu	Ser	Gly	Ile	Thr	340	345	350	
Lys	Gln	Gln	Lys	Leu	Glu	Ala	Ser	Lys	Ser	Phe	His	Lys	Ala	Thr	Leu	355	360	365	
Asp	Val	Asp	Glu	Ala	Gly	Thr	Glu	Ala	Ala	Ala	Ala	Thr	Thr	Phe	Ala	370	375	380	
Ile	Lys	Phe	Phe	Ser	Ala	Gln	Thr	Asn	Arg	His	Ile	Leu	Arg	Phe	Asn	385	390	395	400
Arg	Pro	Phe	Leu	Val	Val	Ile	Phe	Ser	Thr	Ser	Thr	Gln	Ser	Val	Leu	405	410	415	
Phe	Leu	Gly	Lys	Val	Val	Asp	Pro	Thr	Lys	Pro						420	425		

<210> 577  
 <211> 1284  
 <212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (699)..(699)

<223> wherein N is either a "C" or a "T".

<220>

<221> misc\_feature

<222> (1143)..(1143)

<223> wherein N is either a "C" or a "G".

<220>

<221> misc\_feature

<222> (412)..(412)

<223> wherein N is either a "C" or a "T".

<220>

<221> misc\_feature

<222> (597)..(597)

<223> wherein N is either a "T" or a "C".

<400> 577

atgcacctta tcgactacct gctcctcctg ctggttgagac tactggccct ttctcatggc 60  
cagctgcacg ttgagcatga tggtagagagt tgcagtaaca gctcccacca gcagattctg 120  
gagacaggtg agggctcccc cagcctcaag atagcccctg ccaatgctga ctttgccttc 180  
cgcttctact acctgatcgc ttcggagacc ccggggaaga acatcttttt ctccccgctg 240  
agcatctcgg cggcctacgc catgctttcc ctggggggcct gctcacacag ccgcagccag 300  
atccttgagg gcctgggctt caacctcacc gagctgtctg agtccgatgt ccataggggc 360  
ttccagcacc tctgcacac tctcaacctc cccggccatg ggctggaaac angcgtgggc 420  
agtgtctgt tctgagcca caacctgaag ttccttgcaa aattcctgaa tgacaccatg 480  
gccgtctatg aggctaaact cttccacacc aacttctacg aactgtggg cacaatccag 540  
cttatcaacg accacgtcaa gaaggaaact cgagggaaga ttgtggattt ggtcagngag 600  
ctcaagaagg acgtcttgat ggtgctggtg aattacattt acttcaaagc cctgtgggag 660  
aaaccattca tttcctcaag gaccactccc aaagacttnt atgttgatga gaacacaaca 720  
gtccgggtgc ccatgatgct gcaggaccag gagcatcact ggtatcttca tgacagatac 780  
ttgccctgct cggtagctacg gatggattac aaaggagacg caaccgtgtt tttcattctc 840  
cctaaccaag gcaaaatgag ggagattgaa gaggttctga ctccagagat gctaattgagg 900

tggaacaact tgttgcggaag gaggaatttt tacaagaagc tagagttgca tcttcccaag 960  
 ttctccattt ctgggtccta tgtattagat cagattttgc ccaggctggg cttcacggat 1020  
 ctgttctcca agtgggctga cttatccggc atcaccaaac agcaaaaact ggaggcatcc 1080  
 aaaagtttcc acaaggccac cttggacgtg gatgaggctg gcaccgaggg tgcagcagcc 1140  
 acnacgttcg cgatcaaatt cttctctgcc cagaccaatc gccacatcct gcgattcaac 1200  
 cggcccttcc ttgtggtgat cttttccacc agcaccaga gtgtcctctt tctgggcaag 1260  
 gtcgtcgacc ccacgaaacc atag 1284

<210> 578  
 <211> 427  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> VARIANT  
 <222> (138)..(138)  
 <223> wherein Xaa is either "Arg" or a "Cys".

<400> 578

Met	His	Leu	Ile	Asp	Tyr	Leu	Leu	Leu	Leu	Leu	Val	Gly	Leu	Leu	Ala	1	5	10	15
Leu	Ser	His	Gly	Gln	Leu	His	Val	Glu	His	Asp	Gly	Glu	Ser	Cys	Ser	20	25	30	
Asn	Ser	Ser	His	Gln	Gln	Ile	Leu	Glu	Thr	Gly	Glu	Gly	Ser	Pro	Ser	35	40	45	
Leu	Lys	Ile	Ala	Pro	Ala	Asn	Ala	Asp	Phe	Ala	Phe	Arg	Phe	Tyr	Tyr	50	55	60	
Leu	Ile	Ala	Ser	Glu	Thr	Pro	Gly	Lys	Asn	Ile	Phe	Phe	Ser	Pro	Leu	65	70	75	80
Ser	Ile	Ser	Ala	Ala	Tyr	Ala	Met	Leu	Ser	Leu	Gly	Ala	Cys	Ser	His	85	90	95	
Ser	Arg	Ser	Gln	Ile	Leu	Glu	Gly	Leu	Gly	Phe	Asn	Leu	Thr	Glu	Leu	100	105	110	
Ser	Glu	Ser	Asp	Val	His	Arg	Gly	Phe	Gln	His	Leu	Leu	His	Thr	Leu	115	120	125	
Asn	Leu	Pro	Gly	His	Gly	Leu	Glu	Thr	Xaa	Val	Gly	Ser	Ala	Leu	Phe	130	135	140	
Leu	Ser	His	Asn	Leu	Lys	Phe	Leu	Ala	Lys	Phe	Leu	Asn	Asp	Thr	Met	145	150	155	160

Ala	Val	Tyr	Glu	Ala	Lys	Leu	Phe	His	Thr	Asn	Phe	Tyr	Asp	Thr	Val	
				165					170						175	
Gly	Thr	Ile	Gln	Leu	Ile	Asn	Asp	His	Val	Lys	Lys	Glu	Thr	Arg	Gly	
			180					185					190			
Lys	Ile	Val	Asp	Leu	Val	Ser	Glu	Leu	Lys	Lys	Asp	Val	Leu	Met	Val	
		195					200					205				
Leu	Val	Asn	Tyr	Ile	Tyr	Phe	Lys	Ala	Leu	Trp	Glu	Lys	Pro	Phe	Ile	
	210					215					220					
Ser	Ser	Arg	Thr	Thr	Pro	Lys	Asp	Phe	Tyr	Val	Asp	Glu	Asn	Thr	Thr	
225					230					235					240	
Val	Arg	Val	Pro	Met	Met	Leu	Gln	Asp	Gln	Glu	His	His	Trp	Tyr	Leu	
				245					250					255		
His	Asp	Arg	Tyr	Leu	Pro	Cys	Ser	Val	Leu	Arg	Met	Asp	Tyr	Lys	Gly	
			260					265					270			
Asp	Ala	Thr	Val	Phe	Phe	Ile	Leu	Pro	Asn	Gln	Gly	Lys	Met	Arg	Glu	
		275					280					285				
Ile	Glu	Glu	Val	Leu	Thr	Pro	Glu	Met	Leu	Met	Arg	Trp	Asn	Asn	Leu	
	290					295					300					
Leu	Arg	Lys	Arg	Asn	Phe	Tyr	Lys	Lys	Leu	Glu	Leu	His	Leu	Pro	Lys	
305				310						315					320	
Phe	Ser	Ile	Ser	Gly	Ser	Tyr	Val	Leu	Asp	Gln	Ile	Leu	Pro	Arg	Leu	
				325					330					335		
Gly	Phe	Thr	Asp	Leu	Phe	Ser	Lys	Trp	Ala	Asp	Leu	Ser	Gly	Ile	Thr	
			340					345					350			
Lys	Gln	Gln	Lys	Leu	Glu	Ala	Ser	Lys	Ser	Phe	His	Lys	Ala	Thr	Leu	
		355					360					365				
Asp	Val	Asp	Glu	Ala	Gly	Thr	Glu	Ala	Ala	Ala	Ala	Thr	Thr	Phe	Ala	
		370				375						380				
Ile	Lys	Phe	Phe	Ser	Ala	Gln	Thr	Asn	Arg	His	Ile	Leu	Arg	Phe	Asn	
385					390					395					400	
Arg	Pro	Phe	Leu	Val	Val	Ile	Phe	Ser	Thr	Ser	Thr	Gln	Ser	Val	Leu	
				405					410					415		
Phe	Leu	Gly	Lys	Val	Val	Asp	Pro	Thr	Lys	Pro						
			420					425								

<210> 579  
 <211> 18  
 <212> DNA  
 <213> Homo sapiens



<400> 579  
tgtcatcaat ggggtcat

18

<210> 580  
<211> 18  
<212> DNA  
<213> Homo sapiens

<400> 580  
cggcggaggc aggcccgg

18

<210> 581  
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<212> DNA  
<213> Homo sapiens

<400> 581  
gcctgcatcc tgctcctc

18

<210> 582  
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<400> 582  
acgcgggagg aggtcaga

18

<210> 583  
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<212> DNA  
<213> Homo sapiens

<400> 583  
tggagaatgc gtgtatatt

18

<210> 584  
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<212> DNA  
<213> Homo sapiens

<400> 584  
tgtctgttcg tgaggact

18

<210> 585  
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<400> 585  
ccttccttcc gaagagaac

19

<210> 586  
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<212> DNA  
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<400> 586  
aaacacccgc acccaggaa

19

<210> 587  
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<212> DNA  
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<400> 587  
gtacgtggcg taaaagaa

19

<210> 588  
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<400> 588  
atgacatcat taccagcc

19

<210> 589  
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<212> DNA  
<213> Homo sapiens

<400> 589  
catcatcgat gtaatcaca

19

<210> 590  
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<212> DNA  
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<400> 590  
gccagaaagg gggctgcag

19

<210> 591  
<211> 19  
<212> DNA  
<213> Homo sapiens

<400> 591  
caggagaact gccatccag

19

<210> 592  
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<212> DNA  
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<400> 592  
aagtgggaac gactgggca 19

<210> 593  
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<212> DNA  
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<400> 593  
tgaggcatca ttacgcaga 19

<210> 594  
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<400> 594  
aggtgctcat tggctccct 19

<210> 595  
<211> 18  
<212> DNA  
<213> Homo sapiens

<400> 595  
tgaaagaacc acatggcc 18

<210> 596  
<211> 19  
<212> DNA  
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<400> 596  
atcatagata taaatatat 19

<210> 597  
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<212> DNA  
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<400> 597  
agttgacaac tttcacacc 19

<210> 598  
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<212> DNA  
<213> Homo sapiens

<400> 598  
attagtagcc tacctggt

18

<210> 599  
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<212> DNA  
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<400> 599  
gaatgctaata ataaagata

19

<210> 600  
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<212> DNA  
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<400> 600  
agaataatgc ttggcacac

19

<210> 601  
<211> 19  
<212> DNA  
<213> Homo sapiens

<400> 601  
atcagacaca ttttttaggt

19

<210> 602  
<211> 19  
<212> DNA  
<213> Homo sapiens

<400> 602  
gcctgcagat gtcctgtac

19

<210> 603  
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<400> 603  
caaagacttc tatgttgat

19

<210> 604  
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<212> DNA  
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<400> 604  
gagttagaac attag

15

<210> 605  
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<212> DNA  
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<400> 605  
cccacaaact gcttcgg

17

<210> 606  
<211> 21  
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<400> 606  
cttgagctca ctgaccaaat c

21

<210> 607  
<211> 19  
<212> DNA  
<213> Homo sapiens

<400> 607  
gaggatggct atcctcaga

19

<210> 608  
<211> 18  
<212> DNA  
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<400> 608  
tccacaacat ctgtggag

18

<210> 609  
<211> 18  
<212> DNA  
<213> Homo sapiens

<400> 609  
ccaaagttgt ggggatag

18

<210> 610  
<211> 19  
<212> DNA  
<213> Homo sapiens

<400> 610  
tgtttggttg gttgtttgt

19

<210> 611  
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<212> DNA  
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<400> 611  
tgtcatcaac ggggtcat 18

<210> 612  
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<400> 612  
cggcggagac aggcccg 18

<210> 613  
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<400> 613  
gcctgcatcg tgctctc 18

<210> 614  
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<400> 614  
acgcgggaag aggtcaga 18

<210> 615  
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<212> DNA  
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<400> 615  
tggagaatga gtgtattt 18

<210> 616  
<211> 18  
<212> DNA  
<213> Homo sapiens

<400> 616  
tgtctgtttg tgaggact 18

<210> 617  
<211> 19  
<212> DNA  
<213> Homo sapiens

<400> 617  
ccttccttca gaagagaac 19

<210> 618  
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<400> 618  
aaacaccgt acccaggaa 19

<210> 619  
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<212> DNA  
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<400> 619  
gtacgtggca taaaagaa 19

<210> 620  
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<212> DNA  
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<400> 620  
atgacatcac taccagcc 19

<210> 621  
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<400> 621  
catcatcgac gtaatcaca 19

<210> 622  
<211> 19  
<212> DNA  
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<400> 622  
gccagaaaga gggctgcag 19

<210> 623  
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<212> DNA  
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<400> 623  
caggagaacc gccatccag 19

<210> 624  
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 <212> DNA  
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 <400> 624  
 aagtgggaat gactgggca 19

<210> 625  
 <211> 19  
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 <400> 625  
 tgaggcatct ttacgcaga 19

<210> 626  
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 <212> DNA  
 <213> Homo sapiens  
 <400> 626  
 aggtgctcac tggctccct 19

<210> 627  
 <211> 18  
 <212> DNA  
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 <400> 627  
 tgaaagaaac acatggcc 18

<210> 628  
 <211> 19  
 <212> DNA  
 <213> Homo sapiens  
 <400> 628  
 atcatagatg taaatatat 19

<210> 629  
 <211> 19  
 <212> DNA  
 <213> Homo sapiens  
 <400> 629  
 agttgacaag tttcacacc 19

<210> 630  
 <211> 18



<212> DNA  
<213> Homo sapiens

<400> 630  
attagtagct tacctggt

18

<210> 631  
<211> 19  
<212> DNA  
<213> Homo sapiens

<400> 631  
gaatgctaac ataaagata

19

<210> 632  
<211> 19  
<212> DNA  
<213> Homo sapiens

<400> 632  
agaataatgt ttggcacac

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<400> 835

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Trp	Asp	Leu	Leu	His	Arg	Val	Leu	Pro	Thr	Phe	Ile	Ile	Ser	Ile	Cys	35	40	45	
Phe	Phe	Gly	Leu	Leu	Gly	Asn	Leu	Phe	Val	Leu	Leu	Val	Phe	Leu	Leu	50	55	60	
Pro	Arg	Arg	Gln	Leu	Asn	Val	Ala	Glu	Ile	Tyr	Leu	Ala	Asn	Leu	Ala	65	70	75	80
Ala	Ser	Asp	Leu	Val	Phe	Val	Leu	Gly	Leu	Pro	Phe	Trp	Ala	Glu	Asn	85	90	95	
Ile	Trp	Asn	Gln	Phe	Asn	Trp	Pro	Phe	Gly	Ala	Leu	Leu	Cys	Arg	Val	100	105	110	
Ile	Asn	Gly	Val	Ile	Lys	Ala	Asn	Leu	Phe	Ile	Ser	Ile	Phe	Leu	Val	115	120	125	
Val	Ala	Ile	Ser	Gln	Asp	Arg	Tyr	Arg	Val	Leu	Val	His	Pro	Met	Ala	130	135	140	
Ser	Gly	Arg	Gln	Gln	Arg	Arg	Arg	Gln	Ala	Arg	Val	Thr	Cys	Val	Leu	145	150	155	160
Ile	Trp	Val	Val	Gly	Gly	Leu	Leu	Ser	Ile	Pro	Thr	Phe	Leu	Leu	Arg				

165					170					175					
Ser	Ile	Gln	Ala	Val	Pro	Asp	Leu	Asn	Ile	Thr	Ala	Cys	Ile	Leu	Leu
			180					185					190		
Leu	Pro	His	Glu	Ala	Trp	His	Phe	Ala	Arg	Ile	Val	Glu	Leu	Asn	Ile
			195				200					205			
Leu	Gly	Phe	Leu	Leu	Pro	Leu	Ala	Ala	Ile	Val	Phe	Phe	Asn	Tyr	His
	210					215					220				
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225						230					235				240
Arg	Gly	Pro	Lys	Asp	Ser	Lys	Thr	Thr	Ala	Leu	Ile	Leu	Thr	Leu	Val
				245					250					255	
Val	Ala	Phe	Leu	Val	Cys	Trp	Ala	Pro	Tyr	His	Phe	Phe	Ala	Phe	Leu
			260					265					270		
Glu	Phe	Leu	Phe	Gln	Val	Gln	Ala	Val	Arg	Gly	Cys	Phe	Trp	Glu	Asp
			275				280					285			
Phe	Ile	Asp	Leu	Gly	Leu	Gln	Leu	Ala	Asn	Phe	Phe	Ala	Phe	Thr	Asn
	290					295					300				
Ser	Ser	Leu	Asn	Pro	Val	Ile	Tyr	Val	Phe	Val	Gly	Arg	Leu	Phe	Arg
305						310					315				320
Thr	Lys	Val	Trp	Glu	Leu	Tyr	Lys	Gln	Cys	Thr	Pro	Lys	Ser	Leu	Ala
				325					330					335	
Pro	Ile	Ser	Ser	Ser	His	Arg	Lys	Glu	Ile	Phe	Gln	Leu	Phe	Trp	Arg
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 <213> Oryctolagus cuniculus

<400> 836

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			20					25					30		
Asp	Leu	Leu	His	Arg	Leu	Leu	Pro	Thr	Phe	Ile	Ile	Ala	Ile	Phe	Thr
	35						40					45			
Leu	Gly	Leu	Leu	Gly	Asn	Ser	Phe	Val	Leu	Ser	Val	Phe	Leu	Leu	Ala
	50					55					60				

Arg	Arg	Arg	Leu	Ser	Val	Ala	Glu	Ile	Tyr	Leu	Ala	Asn	Leu	Ala	Ala	65	70	75	80
Ser	Asp	Leu	Val	Phe	Val	Leu	Gly	Leu	Pro	Phe	Trp	Ala	Glu	Asn	Val	85	90	95	
Arg	Asn	Gln	Phe	Asp	Trp	Pro	Phe	Gly	Ala	Ala	Leu	Cys	Arg	Ile	Val	100	105	110	
Asn	Gly	Val	Ile	Lys	Ala	Asn	Leu	Phe	Ile	Ser	Ile	Phe	Leu	Val	Val	115	120	125	
Ala	Ile	Ser	Gln	Asp	Arg	Tyr	Ser	Val	Leu	Val	His	Pro	Met	Ala	Ser	130	135	140	
Arg	Arg	Gly	Arg	Arg	Arg	Arg	Gln	Ala	Gln	Ala	Thr	Cys	Ala	Leu	Ile	145	150	155	160
Trp	Leu	Ala	Gly	Gly	Leu	Leu	Ser	Thr	Pro	Thr	Phe	Val	Leu	Arg	Ser	165	170	175	
Val	Arg	Ala	Val	Pro	Glu	Leu	Asn	Val	Ser	Ala	Cys	Ile	Leu	Leu	Leu	180	185	190	
Pro	His	Glu	Ala	Trp	His	Trp	Leu	Arg	Met	Val	Glu	Leu	Asn	Leu	Leu	195	200	205	
Gly	Phe	Leu	Leu	Pro	Leu	Ala	Ala	Ile	Leu	Phe	Phe	Asn	Cys	His	Ile	210	215	220	
Leu	Ala	Ser	Leu	Arg	Arg	Arg	Gly	Glu	Arg	Val	Pro	Ser	Arg	Cys	Gly	225	230	235	240
Gly	Pro	Arg	Asp	Ser	Lys	Ser	Thr	Ala	Leu	Ile	Leu	Thr	Leu	Val	Ala	245	250	255	
Ser	Phe	Leu	Val	Cys	Trp	Ala	Pro	Tyr	His	Phe	Phe	Ala	Phe	Leu	Glu	260	265	270	
Cys	Leu	Trp	Gln	Val	His	Ala	Ile	Gly	Gly	Cys	Phe	Trp	Glu	Glu	Phe	275	280	285	
Thr	Asp	Leu	Gly	Leu	Gln	Leu	Ser	Asn	Phe	Ser	Ala	Phe	Val	Asn	Ser	290	295	300	
Cys	Leu	Asn	Pro	Val	Ile	Tyr	Val	Phe	Val	Gly	Arg	Leu	Phe	Arg	Thr	305	310	315	320
Lys	Val	Trp	Glu	Leu	Cys	Gln	Gln	Cys	Ser	Pro	Arg	Ser	Leu	Ala	Pro	325	330	335	
Val	Ser	Ser	Ser	Arg	Arg	Lys	Glu	Met	Leu	Trp	Gly	Phe	Trp	Arg	Asn	340	345	350	
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<213> Rattus norvegicus

<400> 837

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Asp Leu Leu Tyr Arg Val Leu Pro Gly Phe Val Ile Thr Ile Cys Phe  
35 40 45  
Phe Gly Leu Leu Gly Asn Leu Val Leu Ser Phe Phe Leu Leu Pro  
50 55 60  
Trp Arg Gln Trp Trp Trp Gln Gln Arg Gln Arg Gln Gln Arg Leu Thr  
65 70 75 80  
Ile Ala Glu Ile Tyr Leu Ala Asn Leu Ala Ala Ser Asp Leu Val Phe  
85 90 95  
Val Leu Gly Leu Pro Phe Trp Ala Glu Asn Ile Gly Asn Arg Phe Asn  
100 105 110  
Trp Pro Phe Gly Thr Asp Leu Cys Arg Val Val Ser Gly Val Ile Lys  
115 120 125  
Ala Asn Leu Phe Val Ser Ile Phe Leu Val Val Ala Ile Ser Gln Asp  
130 135 140  
Arg Tyr Arg Leu Leu Val Tyr Pro Met Thr Ser Trp Gly Tyr Arg Arg  
145 150 155 160  
Arg Arg Gln Ala Gln Ala Thr Cys Leu Leu Ile Trp Val Ala Gly Gly  
165 170 175  
Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg Ser Val Lys Val Val Pro  
180 185 190  
Asp Leu Asn Val Ser Ala Cys Ile Leu Leu Phe Pro His Glu Ala Trp  
195 200 205  
His Phe Ala Arg Met Val Glu Leu Asn Val Leu Gly Phe Leu Leu Pro  
210 215 220  
Val Thr Ala Ile Ile Phe Phe Asn Tyr His Ile Leu Ala Ser Leu Arg  
225 230 235 240  
Gly Gln Lys Glu Ala Ser Arg Thr Arg Cys Gly Gly Pro Lys Gly Ser  
245 250 255  
Lys Thr Thr Gly Leu Ile Leu Thr Leu Val Ala Ser Phe Leu Val Cys  
260 265 270  
Trp Cys Pro Tyr His Phe Phe Ala Phe Leu Asp Phe Leu Val Gln Val  
275 280 285

Arg Val Ile Gln Asp Cys Ser Trp Lys Glu Ile Thr Asp Leu Gly Leu  
 290 295 300

Gln Leu Ala Asn Phe Phe Ala Phe Val Asn Ser Cys Leu Asn Pro Leu  
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Leu

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 35 40 45

Pro Asp Thr Glu Trp Trp Ser Trp Leu Asn Ala Ile Gln Ala Pro Phe  
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Leu Trp Val Leu Phe Leu Leu Ala Ala Leu Glu Asn Leu Phe Val Leu  
 65 70 75 80

Ser Val Phe Phe Leu His Lys Asn Ser Cys Thr Val Ala Glu Ile Tyr  
 85 90 95

Leu Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro  
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Phe Trp Ala Ile Thr Ile Ala Asn Asn Phe Asp Trp Val Phe Gly Glu  
 115 120 125

Val Leu Cys Arg Val Val Asn Thr Met Ile Tyr Met Asn Leu Tyr Ser  
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Ser Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg Tyr Leu Ala Leu  
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Val Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys  
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Leu Tyr Ser Leu Val Ile Trp Gly Cys Thr Leu Leu Leu Ser Ser Pro  
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Met Leu Val Phe Arg Thr Met Arg Glu Tyr Ser Glu Glu Gly His Asn

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Val	Thr	Ala	Cys	Val	Ile	Val	Tyr	Pro	Ser	Arg	Ser	Trp	Glu	Val	Phe
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Thr	Asn	Val	Leu	Leu	Asn	Leu	Val	Gly	Phe	Leu	Leu	Pro	Leu	Ser	Val
225					230					235					240
Ile	Thr	Phe	Cys	Thr	Val	Arg	Ile	Leu	Gln	Val	Leu	Arg	Asn	Asn	Glu
				245					250					255	
Met	Lys	Lys	Phe	Lys	Glu	Val	Gln	Thr	Glu	Arg	Lys	Ala	Thr	Val	Leu
			260					265					270		
Val	Leu	Ala	Val	Leu	Gly	Leu	Phe	Val	Leu	Cys	Trp	Val	Pro	Phe	Gln
		275					280					285			
Ile	Ser	Thr	Phe	Leu	Asp	Thr	Leu	Leu	Arg	Leu	Gly	Val	Leu	Ser	Gly
	290					295					300				
Cys	Trp	Asp	Glu	His	Ala	Val	Asp	Val	Ile	Thr	Gln	Ile	Ser	Ser	Tyr
305					310					315					320
Val	Ala	Tyr	Ser	Asn	Ser	Gly	Leu	Asn	Pro	Leu	Val	Tyr	Val	Ile	Val
				325					330					335	
Gly	Lys	Arg	Phe	Arg	Lys	Lys	Ser	Arg	Glu	Val	Tyr	Arg	Val	Leu	Cys
			340					345					350		
Gln	Lys	Gly	Gly	Cys	Met	Gly	Glu	Pro	Val	Gln	Met	Glu	Asn	Ser	Met
		355					360					365			
Gly	Thr	Leu	Arg	Thr	Ser	Ile	Ser	Val	Glu	Arg	Gln	Ile	His	Lys	Leu
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			20					25					30		
Asn	Val	Ile	Gln	Ala	Pro	Phe	Leu	Trp	Val	Leu	Phe	Val	Leu	Ala	Thr
		35					40					45			
Leu	Glu	Asn	Leu	Phe	Val	Leu	Ser	Val	Phe	Cys	Leu	His	Lys	Ser	Ser
	50					55					60				

Cys Thr Val Ala Glu Val Tyr Leu Gly Asn Leu Ala Ala Ala Asp Leu  
 65 70 75 80  
 Ile Leu Ala Cys Gly Leu Pro Phe Trp Ala Val Thr Ile Ala Asn His  
 85 90 95  
 Phe Asp Trp Leu Phe Gly Glu Ala Leu Cys Arg Val Val Asn Thr Met  
 100 105 110  
 Ile Tyr Met Asn Leu Tyr Ser Ser Ile Cys Phe Leu Met Leu Val Ser  
 115 120 125  
 Ile Asp Arg Tyr Leu Ala Leu Val Lys Thr Met Ser Ile Gly Arg Met  
 130 135 140  
 Arg Arg Val Arg Trp Ala Lys Leu Tyr Ser Leu Val Ile Trp Gly Cys  
 145 150 155 160  
 Thr Leu Leu Leu Ser Ser Pro Met Leu Val Phe Arg Thr Met Lys Asp  
 165 170 175  
 Tyr Arg Asp Glu Gly Tyr Asn Val Thr Ala Cys Ile Ile Asp Tyr Pro  
 180 185 190  
 Ser Arg Ser Trp Glu Val Phe Thr Asn Val Leu Leu Asn Leu Val Gly  
 195 200 205  
 Phe Leu Leu Pro Leu Ser Val Ile Thr Phe Cys Thr Val Gln Ile Leu  
 210 215 220  
 Gln Val Leu Arg Asn Asn Glu Met Gln Lys Phe Lys Glu Ile Gln Thr  
 225 230 235 240  
 Glu Arg Arg Ala Thr Val Leu Val Leu Ala Val Leu Leu Leu Phe Val  
 245 250 255  
 Val Cys Trp Leu Pro Phe Gln Val Ser Thr Phe Leu Asp Thr Leu Leu  
 260 265 270  
 Lys Leu Gly Val Leu Ser Ser Cys Trp Asp Glu His Val Ile Asp Val  
 275 280 285  
 Ile Thr Gln Val Gly Ser Phe Met Gly Tyr Ser Asn Ser Cys Leu Asn  
 290 295 300  
 Pro Leu Val Tyr Val Ile Val Gly Lys Arg Phe Arg Lys Lys Ser Arg  
 305 310 315 320  
 Glu Val Tyr Arg Ala Ala Cys Pro Lys Ala Gly Cys Val Leu Glu Pro  
 325 330 335  
 Val Gln Ala Glu Ser Ser Met Gly Thr Leu Arg Thr Ser Ile Ser Val  
 340 345 350  
 Glu Arg Gln Ile His Lys Leu Pro Glu Trp Thr Arg Ser Ser Gln  
 355 360 365

<210> 840  
 <211> 372  
 <212> PRT  
 <213> Cavia porcellus

<400> 840

Met	Phe	Asn	Ile	Thr	Ser	Gln	Val	Ser	Ala	Leu	Asn	Ala	Thr	Leu	Ala	1	5	10	15
Gln	Gly	Asn	Ser	Cys	Leu	Asp	Ala	Glu	Trp	Trp	Ser	Trp	Leu	Asn	Thr	20	25	30	
Ile	Gln	Ala	Pro	Phe	Leu	Trp	Val	Leu	Phe	Val	Leu	Ala	Val	Leu	Glu	35	40	45	
Asn	Ile	Phe	Val	Leu	Ser	Val	Phe	Phe	Leu	His	Lys	Ser	Ser	Cys	Thr	50	55	60	
Val	Ala	Glu	Ile	Tyr	Leu	Gly	Asn	Leu	Ala	Val	Ala	Asp	Leu	Ile	Leu	65	70	75	80
Ala	Phe	Gly	Leu	Pro	Phe	Trp	Ala	Ile	Thr	Ile	Ala	Asn	Asn	Phe	Asp	85	90	95	
Trp	Leu	Phe	Gly	Glu	Val	Leu	Cys	Arg	Met	Val	Asn	Thr	Met	Ile	Gln	100	105	110	
Met	Asn	Met	Tyr	Ser	Ser	Ile	Cys	Phe	Leu	Met	Leu	Val	Ser	Ile	Asp	115	120	125	
Arg	Tyr	Leu	Ala	Leu	Val	Lys	Thr	Met	Ser	Met	Gly	Arg	Met	Arg	Gly	130	135	140	
Val	Arg	Trp	Ala	Lys	Leu	Tyr	Ser	Leu	Val	Ile	Trp	Gly	Cys	Ala	Leu	145	150	155	160
Leu	Leu	Ser	Ser	Pro	Met	Leu	Val	Phe	Arg	Thr	Met	Lys	Asp	Tyr	Arg	165	170	175	
Asp	Glu	Gly	His	Asn	Val	Thr	Ala	Cys	Leu	Ile	Ile	Tyr	Pro	Ser	Leu	180	185	190	
Thr	Trp	Gln	Val	Phe	Thr	Asn	Val	Leu	Leu	Asn	Leu	Val	Gly	Phe	Leu	195	200	205	
Leu	Pro	Leu	Ser	Ile	Ile	Thr	Phe	Cys	Thr	Val	Gln	Ile	Met	Gln	Val	210	215	220	
Leu	Arg	Asn	Asn	Glu	Met	Gln	Lys	Phe	Lys	Glu	Ile	Gln	Thr	Glu	Arg	225	230	235	240
Arg	Ala	Thr	Val	Leu	Val	Leu	Ala	Val	Leu	Leu	Leu	Phe	Val	Val	Cys	245	250	255	
Trp	Leu	Pro	Phe	Gln	Ile	Gly	Thr	Phe	Leu	Asp	Thr	Leu	Arg	Leu	Leu	260	265	270	



Gly Phe Leu Pro Gly Cys Trp Glu His Val Ile Asp Leu Ile Thr Gln  
275 280 285

Ile Ser Ser Tyr Leu Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val  
290 295 300

Tyr Val Ile Val Gly Lys Arg Phe Arg Lys Lys Ser Arg Glu Val Tyr  
305 310 315 320

His Gly Leu Cys Arg Ser Gly Gly Cys Val Ser Glu Pro Ala Gln Ser  
325 330 335

Glu Asn Ser Met Gly Thr Leu Arg Thr Ser Ile Ser Val Asp Arg Gln  
340 345 350

Ile His Lys Leu Gln Asp Trp Ala Arg Ser Ser Ser Glu Gly Thr Pro  
355 360 365

Pro Gly Leu Leu  
370

<210> 841  
<211> 396  
<212> PRT  
<213> Rattus norvegicus

<400> 841

Met Asp Thr Arg Ser Ser Leu Cys Pro Lys Thr Gln Ala Val Val Ala  
1 5 10 15

Val Phe Trp Gly Pro Gly Cys His Leu Ser Thr Cys Ile Glu Met Phe  
20 25 30

Asn Ile Thr Thr Gln Ala Leu Gly Ser Ala His Asn Gly Thr Phe Ser  
35 40 45

Glu Val Asn Cys Pro Asp Thr Glu Trp Trp Ser Trp Leu Asn Ala Ile  
50 55 60

Gln Ala Pro Phe Leu Trp Val Leu Phe Leu Leu Ala Ala Leu Glu Asn  
65 70 75 80

Ile Phe Val Leu Ser Val Phe Cys Leu His Lys Thr Asn Cys Thr Val  
85 90 95

Ala Glu Ile Tyr Leu Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala  
100 105 110

Cys Gly Leu Pro Phe Trp Ala Ile Thr Ile Ala Asn Asn Phe Asp Trp  
115 120 125

Leu Phe Gly Glu Val Leu Cys Arg Val Val Asn Thr Met Ile Tyr Met  
130 135 140

Asn Leu Tyr Ser Ser Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg

145	150	155	160
Tyr Leu Ala Leu Val Lys Thr Met Ser Met Gly Arg Met Arg Gly Val	165	170	175
Arg Trp Ala Lys Leu Tyr Ser Leu Val Ile Trp Ser Cys Thr Leu Leu	180	185	190
Leu Ser Ser Pro Met Leu Val Phe Arg Thr Met Lys Asp Tyr Arg Glu	195	200	205
Glu Gly His Asn Val Thr Ala Cys Val Ile Val Tyr Pro Ser Arg Ser	210	215	220
Trp Glu Val Phe Thr Asn Met Leu Leu Asn Leu Val Gly Phe Leu Leu	225	230	235
Pro Leu Ser Ile Ile Thr Phe Cys Thr Val Arg Ile Met Gln Val Leu	245	250	255
Arg Asn Asn Glu Met Lys Lys Phe Lys Glu Val Gln Thr Glu Lys Lys	260	265	270
Ala Thr Val Leu Val Leu Ala Val Leu Gly Leu Phe Val Leu Cys Trp	275	280	285
Phe Pro Phe Gln Ile Ser Thr Phe Leu Asp Thr Leu Leu Arg Leu Gly	290	295	300
Val Leu Ser Gly Cys Trp Asn Glu Arg Ala Val Asp Ile Val Thr Gln	305	310	315
Ile Ser Ser Tyr Val Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val	325	330	335
Tyr Val Ile Val Gly Lys Arg Phe Arg Lys Lys Ser Arg Glu Val Tyr	340	345	350
Gln Ala Ile Cys Arg Lys Gly Gly Cys Met Gly Glu Ser Val Gln Met	355	360	365
Glu Asn Ser Met Gly Thr Leu Arg Thr Ser Ile Ser Val Asp Arg Gln	370	375	380
Ile His Lys Leu Gln Asp Trp Ala Gly Asn Lys Gln	385	390	395

<210> 842  
 <211> 3405  
 <212> DNA  
 <213> homo sapiens  
  
 <220>  
 <221> misc\_feature  
 <222> (2173)..(2173)  
 <223> wherein N is either a "T" or a "C".

<400> 842

cgcccaaccc aagttcaaag gctgataaga gagaaaatct catgaggagg ttttagtcta	60
gggaaagtca ttcagtggat gtgatcttgg ctacacagggg acgatgtcaa gctcttcctg	120
gctccttctc agccttggtg ctgtaactgc tgctcagtc accattgagg aacaggccaa	180
gacatttttg gacaagttta accacgaagc cgaagacctg ttctatcaaa gttcacttgc	240
ttcttggaat tataacacca atattactga agagaatgtc caaaacatga ataatgctgg	300
ggacaaatgg tctgcctttt taaaggaaca gtccacactt gcccaaagt atccactaca	360
agaaattcag aatctcacag tcaagcttca gctgcaggct cttcagcaaa atgggtcttc	420
agtgtcttca gaagacaaga gcaaacggtt gaacacaatt ctaaatacaa tgagcaccat	480
ctacagtact ggaaaagttt gtaaccaga taatccacaa gaatgcttat tacttgaacc	540
aggtttgaat gaaataatgg caaacagttt agactacaat gagaggctct gggcttggga	600
aagctggaga tctgaggtcg gcaagcagct gaggccatta tatgaagagt atgtggtctt	660
gaaaaatgag atggcaagag caaatcatta tgaggactat ggggattatt ggagaggaga	720
ctatgaagta aatggggtag atggctatga ctacagccgc ggccagttga ttgaagatgt	780
ggaacatacc tttgaagaga ttaaaccatt atatgaacat cttcatgcct atgtgagggc	840
aaagttgatg aatgcctatc cttcctatat cagtccaatt ggatgcctcc ctgctcattt	900
gcttgggtgat atgtggggta gattttggac aaatctgtac tctttgacag ttccctttgg	960
acagaaacca aacatagatg ttactgatgc aatgggtggac caggcctggg atgcacagag	1020
aatattcaag gaggcgaga agttctttgt atctgttgggt cttcctaata tgactcaagg	1080
attctgggaa aattccatgc taacggaccc aggaaatgtt cagaaagcag tctgccatcc	1140
cacagcttgg gacctgggga agggcgactt caggatcctt atgtgcacaa aggtgacaat	1200
ggacgacttc ctgacagctc atcatgagat ggggcatatc cagtatgata tggcatatgc	1260
tgcacaacct tttctgctaa gaaatggagc taatgaagga ttccatgaag ctgttgggga	1320
aatcatgtca ctttctgcag ccacacctaa gcatttaaaa tccattggtc ttctgtcacc	1380
cgattttcaa gaagacaatg aaacagaaat aaacttcctg ctcaaacaag cactcacgat	1440
tgttgggact ctgccattta cttacatggt agagaagtgg aggtggatgg tctttaag	1500
ggaaattccc aaagaccagt ggatgaaaaa gtgggtgggag atgaagcgag agatagttgg	1560
ggtgggtgaa cctgtgcccc atgatgaaac atactgtgac ccgcacatctc tgttccatgt	1620
ttctaattgat tactcattca ttcgatatta cacaaggacc ctttaccaat tccagtttca	1680



cagacactca ataaatgcta gatttacaca ctcaaaaaaa aaaaa

3405

<210> 843  
<211> 805  
<212> PRT  
<213> homo sapiens

<400> 843

Met Ser Ser Ser Ser Trp Leu Leu Leu Ser Leu Val Ala Val Thr Ala  
1 5 10 15

Ala Gln Ser Thr Ile Glu Glu Gln Ala Lys Thr Phe Leu Asp Lys Phe  
20 25 30

Asn His Glu Ala Glu Asp Leu Phe Tyr Gln Ser Ser Leu Ala Ser Trp  
35 40 45

Asn Tyr Asn Thr Asn Ile Thr Glu Glu Asn Val Gln Asn Met Asn Asn  
50 55 60

Ala Gly Asp Lys Trp Ser Ala Phe Leu Lys Glu Gln Ser Thr Leu Ala  
65 70 75 80

Gln Met Tyr Pro Leu Gln Glu Ile Gln Asn Leu Thr Val Lys Leu Gln  
85 90 95

Leu Gln Ala Leu Gln Gln Asn Gly Ser Ser Val Leu Ser Glu Asp Lys  
100 105 110

Ser Lys Arg Leu Asn Thr Ile Leu Asn Thr Met Ser Thr Ile Tyr Ser  
115 120 125

Thr Gly Lys Val Cys Asn Pro Asp Asn Pro Gln Glu Cys Leu Leu Leu  
130 135 140

Glu Pro Gly Leu Asn Glu Ile Met Ala Asn Ser Leu Asp Tyr Asn Glu  
145 150 155 160

Arg Leu Trp Ala Trp Glu Ser Trp Arg Ser Glu Val Gly Lys Gln Leu  
165 170 175

Arg Pro Leu Tyr Glu Glu Tyr Val Val Leu Lys Asn Glu Met Ala Arg  
180 185 190

Ala Asn His Tyr Glu Asp Tyr Gly Asp Tyr Trp Arg Gly Asp Tyr Glu  
195 200 205

Val Asn Gly Val Asp Gly Tyr Asp Tyr Ser Arg Gly Gln Leu Ile Glu  
210 215 220

Asp Val Glu His Thr Phe Glu Glu Ile Lys Pro Leu Tyr Glu His Leu  
225 230 235 240

His Ala Tyr Val Arg Ala Lys Leu Met Asn Ala Tyr Pro Ser Tyr Ile  
245 250 255

Ser Pro Ile Gly Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly  
 260 265 270  
 Arg Phe Trp Thr Asn Leu Tyr Ser Leu Thr Val Pro Phe Gly Gln Lys  
 275 280 285  
 Pro Asn Ile Asp Val Thr Asp Ala Met Val Asp Gln Ala Trp Asp Ala  
 290 295 300  
 Gln Arg Ile Phe Lys Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu  
 305 310 315 320  
 Pro Asn Met Thr Gln Gly Phe Trp Glu Asn Ser Met Leu Thr Asp Pro  
 325 330 335  
 Gly Asn Val Gln Lys Ala Val Cys His Pro Thr Ala Trp Asp Leu Gly  
 340 345 350  
 Lys Gly Asp Phe Arg Ile Leu Met Cys Thr Lys Val Thr Met Asp Asp  
 355 360 365  
 Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala  
 370 375 380  
 Tyr Ala Ala Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe  
 385 390 395 400  
 His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys  
 405 410 415  
 His Leu Lys Ser Ile Gly Leu Leu Ser Pro Asp Phe Gln Glu Asp Asn  
 420 425 430  
 Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly  
 435 440 445  
 Thr Leu Pro Phe Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe  
 450 455 460  
 Lys Gly Glu Ile Pro Lys Asp Gln Trp Met Lys Lys Trp Trp Glu Met  
 465 470 475 480  
 Lys Arg Glu Ile Val Gly Val Val Glu Pro Val Pro His Asp Glu Thr  
 485 490 495  
 Tyr Cys Asp Pro Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe  
 500 505 510  
 Ile Arg Tyr Tyr Thr Arg Thr Leu Tyr Gln Phe Gln Phe Gln Glu Ala  
 515 520 525  
 Leu Cys Gln Ala Ala Lys His Glu Gly Pro Leu His Lys Cys Asp Ile  
 530 535 540  
 Ser Asn Ser Thr Glu Ala Gly Gln Lys Leu Phe Asn Met Leu Arg Leu  
 545 550 555 560

Gly Lys Ser Glu Pro Trp Thr Leu Ala Leu Glu Asn Val Val Gly Ala  
 565 570 575  
 Lys Asn Met Asn Val Arg Pro Leu Leu Asn Tyr Phe Glu Pro Leu Phe  
 580 585 590  
 Thr Trp Leu Lys Asp Gln Asn Lys Asn Ser Phe Val Gly Trp Ser Thr  
 595 600 605  
 Asp Trp Ser Pro Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu  
 610 615 620  
 Lys Ser Ala Leu Gly Asp Lys Ala Tyr Glu Trp Asn Asp Asn Glu Met  
 625 630 635 640  
 Tyr Leu Phe Arg Ser Ser Val Ala Tyr Ala Met Arg Gln Tyr Phe Leu  
 645 650 655  
 Lys Val Lys Asn Gln Met Ile Leu Phe Gly Glu Glu Asp Val Arg Val  
 660 665 670  
 Ala Asn Leu Lys Pro Arg Ile Ser Phe Asn Phe Phe Val Thr Ala Pro  
 675 680 685  
 Lys Asn Val Ser Asp Ile Ile Pro Arg Thr Glu Val Glu Lys Ala Ile  
 690 695 700  
 Arg Met Ser Arg Ser Arg Ile Asn Asp Ala Phe Arg Leu Asn Asp Asn  
 705 710 715 720  
 Ser Leu Glu Phe Leu Gly Ile Gln Pro Thr Leu Gly Pro Pro Asn Gln  
 725 730 735  
 Pro Pro Val Ser Ile Trp Leu Ile Val Phe Gly Val Val Met Gly Val  
 740 745 750  
 Ile Val Val Gly Ile Val Ile Leu Ile Phe Thr Gly Ile Arg Asp Arg  
 755 760 765  
 Lys Lys Lys Asn Lys Ala Arg Ser Gly Glu Asn Pro Tyr Ala Ser Ile  
 770 775 780  
 Asp Ile Ser Lys Gly Glu Asn Asn Pro Gly Phe Gln Asn Thr Asp Asp  
 785 790 795 800  
 Val Gln Thr Ser Phe  
 805

<210> 844  
 <211> 3733  
 <212> DNA  
 <213> homo sapiens  
 <220>  
 <221> misc\_feature  
 <222> (40)..(40)

<223> wherein N is either a "C" or a "T".

<220>

<221> misc\_feature

<222> (47)..(47)

<223> wherein N is either an "A" or a "C".

<220>

<221> misc\_feature

<222> (933)..(933)

<223> wherein N is either a "T" or a "C".

<220>

<221> misc\_feature

<222> (1061)..(1061)

<223> wherein N is either a "G" or an "A".

<400> 844

atgttctctc cctggaagat atcaatgttt ctgtctgttn gtgaggnctc cgtgcccacc 60  
acggcctctt tcagcgccga catgctcaat gtcaccttgc aagggcccac tcttaacggg 120  
acctttgccc agagcaaagt cccccaagt gagtggctgg gctggctcaa caccatccag 180  
cccccttcc tctgggtgct gttcgtgctg gccaccctag agaacatctt tgtcctcagc 240  
gttctctgcc tgcacaagag cagctgcacg gtggcagaga tctacctggg gaacctggcc 300  
gcagcagacc tgatcctggc ctgcgggctg cccttctggg ccatcaccat ctccaacaac 360  
ttcgactggc tctttgggga gacgctctgc cgcgtggtga atgccattat ctccatgaac 420  
ctgtacagca gcatctgttt cctgatgctg gtgagcatcg accgctacct ggccctgggtg 480  
aaaaccatgt ccatggggccg gatgcgcggc gtgcgctggg ccaagctcta cagcttgggtg 540  
atctgggggt gtacgctgct cctgagctca cccatgctgg tgttccggac catgaaggag 600  
tacagcgatg agggccacaa cgtcaccgct tgtgtcatca gctaccatc cctcatctgg 660  
gaagtgttca ccaacatgct cctgaatgtc gtgggcttcc tgctgcccct gagtgtcatc 720  
accttctgca cgatgcagat catgcagggtg ctgcggaaca acgagatgca gaagttcaag 780  
gagatccaga cggagaggag ggccacgggtg ctagtctctgg ttgtgctgct gctattcatc 840  
atctgctggc tgcccttcca gatcagcacc ttcttgata cgtgcatcg cctcggcatc 900  
ctctccagct gccaggacga gcgcatcatc gangtaatca cacagatcgc ctcttcatg 960  
gcctacagca acagctgcct caaccactg gtgtacgtga tcgtgggcaa gcgcttccga 1020  
aagaagtctt gggaggtgta ccaggagtg tgccagaaag ngggctgcag gtcagaacct 1080



1140  
 1200  
 1260  
 1320  
 1380  
 1440  
 1500  
 1560  
 1620  
 1680  
 1740  
 1800  
 1860  
 1920  
 1980  
 2040  
 2100  
 2160  
 2220  
 2280  
 2340  
 2400  
 2460  
 2520  
 2580  
 2640  
 2700  
 2760

attcagatgg	agaactccat	gggcacactg	cggacctcca	tctccgtgga	acgccagatt	1140
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gccaaggact	ccaaaatcac	aacagcatta	ctgttcttat	ttgctgccac	acctgagcca	1440
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tgagcactgt	aggcaagacc	caagaaagag	aaggagccat	ctccatcttg	aaggaactca	1860
aagactcaag	tgggaacgac	tggggcactgc	caccaccaga	aagctgttcg	acgagacggt	1920
cgagcagggg	gctgtgggtg	atatggacag	cagaaggggg	agaccaaggt	tccagctcaa	1980
ccaataacta	ttgcacaacc	acctgtccct	gcctcagttc	ccttttatgt	aacatgaagt	2040
cgttgtgagg	gttaaaggca	gtaacaggta	taaagtactt	agaaaagcaa	aggggtgctac	2100
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acagtgtga	gacccccac	caccagccgg	tacctgggaa	gggggagagt	gcaggcctgc	2460
tcagggactg	ttcctgtctc	agcaaccaag	ggattgttcc	tgtcaatcaa	tggtttattg	2520
gaaggtggcc	cagtatgagc	cctagaagag	tgtgaaaagg	aatggcaatg	gtgttcacca	2580
tcggcagtgc	cagggcagca	ctcattcact	tgataaatga	atatttatta	gctgggttga	2640
gagctagaac	ctggagagct	agaacctgga	gaactagaac	ctggagggct	agaacctgga	2700
gaggctagaa	ccaagaaggg	ctagaacctg	gaggggctag	aacctagaga	agctaaaacc	2760

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aagggctaga acctggaggg ctggaatctg gagagctaga acctggaggg ctagaacctg	2940
gagggctaga acctagaagg gctagaacct ggagggctag aacctggcag gttagaacct	3000
agaagggcta gaacctggag agccagaacc tggagggcta gaacctggaa gggctagaac	3060
ctgtagagct agaacatgga gagctagaac ccggcaggct agaacctggc aagctagaac	3120
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gagcccataa atcctgacca atccaactct gaattttaaa gcaaaagcgt gaaaaaaaaag	3240
attccctcct tcccccaac ccactctttt ttcccaccac ccactctcct ctgcctcagt	3300
aagtatctgg aggaagaaaa caggtgaaag aagaagtaaa aaccatttag tattagtatt	3360
agaatgaagt caaactgtgc cacacatggt gaatgaaaaa aaaaaaaaaag aggctgtgtt	3420
ttgtcacaca gggcagtcac tcagcaccag agcacgtgat ggtctgagac tctcttagga	3480
gcagagctct gccgcaatgg ccatgtgggg atccacacct ggtctgaggg gcaactgagt	3540
ctgcgggaga agagcggccc tatgcatggt gtagatgcc tgataaagaa catctgtcct	3600
gtgaaagact caatgagctg ttatgttgta aacaggaagc atttcacatc caaacgagaa	3660
aatcatgtaa acatgtgtct tttctgtaga gcataataaa tggatgaggt ttttgcaaaa	3720
aaaaaaaaaa aaa	3733

<210> 845  
 <211> 391  
 <212> PRT  
 <213> homo sapiens

<220>  
 <221> VARIANT  
 <222> (14)..(14)  
 <223> wherein Xaa is either "Arg" or a "Cys".

<220>  
 <221> VARIANT  
 <222> (16)..(16)  
 <223> wherein Xaa is either "Asp" or a "Ala".

<220>  
 <221> VARIANT  
 <222> (354)..(354)  
 <223> wherein Xaa is either "Gly" or a "Glu".

<400> 845

Met Phe Ser Pro Trp Lys Ile Ser Met Phe Leu Ser Val Xaa Glu Xaa  
1 5 10 15  
Ser Val Pro Thr Thr Ala Ser Phe Ser Ala Asp Met Leu Asn Val Thr  
20 25 30  
Leu Gln Gly Pro Thr Leu Asn Gly Thr Phe Ala Gln Ser Lys Cys Pro  
35 40 45  
Gln Val Glu Trp Leu Gly Trp Leu Asn Thr Ile Gln Pro Pro Phe Leu  
50 55 60  
Trp Val Leu Phe Val Leu Ala Thr Leu Glu Asn Ile Phe Val Leu Ser  
65 70 75 80  
Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu  
85 90 95  
Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe  
100 105 110  
Trp Ala Ile Thr Ile Ser Asn Asn Phe Asp Trp Leu Phe Gly Glu Thr  
115 120 125  
Leu Cys Arg Val Val Asn Ala Ile Ile Ser Met Asn Leu Tyr Ser Ser  
130 135 140  
Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg Tyr Leu Ala Leu Val  
145 150 155 160  
Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys Leu  
165 170 175  
Tyr Ser Leu Val Ile Trp Gly Cys Thr Leu Leu Leu Ser Ser Pro Met  
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Leu Val Phe Arg Thr Met Lys Glu Tyr Ser Asp Glu Gly His Asn Val  
195 200 205  
Thr Ala Cys Val Ile Ser Tyr Pro Ser Leu Ile Trp Glu Val Phe Thr  
210 215 220  
Asn Met Leu Leu Asn Val Val Gly Phe Leu Leu Pro Leu Ser Val Ile  
225 230 235 240  
Thr Phe Cys Thr Met Gln Ile Met Gln Val Leu Arg Asn Asn Glu Met  
245 250 255  
Gln Lys Phe Lys Glu Ile Gln Thr Glu Arg Arg Ala Thr Val Leu Val  
260 265 270  
Leu Val Val Leu Leu Leu Phe Ile Ile Cys Trp Leu Pro Phe Gln Ile  
275 280 285

Ser Thr Phe Leu Asp Thr Leu His Arg Leu Gly Ile Leu Ser Ser Cys  
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Gln Asp Glu Arg Ile Ile Asp Val Ile Thr Gln Ile Ala Ser Phe Met  
 305 310 315 320

Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val Tyr Val Ile Val Gly  
 325 330 335

Lys Arg Phe Arg Lys Lys Ser Trp Glu Val Tyr Gln Gly Val Cys Gln  
 340 345 350

Lys Xaa Gly Cys Arg Ser Glu Pro Ile Gln Met Glu Asn Ser Met Gly  
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Asp Trp Ala Gly Ser Arg Gln  
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<212> PRT  
<213> homo sapiens  
<400> 847

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Val Arg Asn Cys Ser Thr Asn Pro Pro Tyr Leu Pro Val Thr Val Val  
35 40 45  
Asn Thr Thr Met Ser Leu Thr Ala Leu Arg Gln Gln Met Gln Thr Gln  
50 55 60  
Asn Leu Ser Ala Tyr Ile Ile Pro Gly Thr Asp Ala His Met Asn Glu  
65 70 75 80  
Tyr Ile Gly Gln His Asp Glu Arg Arg Ala Trp Ile Thr Gly Phe Thr  
85 90 95  
Gly Ser Ala Gly Thr Ala Val Val Thr Met Lys Lys Ala Ala Val Trp  
100 105 110

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Trp	Glu	Leu	His	Lys	Glu	Val	Gly	Thr	Thr	Pro	Ile	Val	Thr	Trp	Leu		
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Asn	Arg	Gln	Leu	Val	Ser	Ile	Thr	Thr	Asn	Leu	Val	Asp	Leu	Val	Trp		
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Gly	Ser	Glu	Arg	Pro	Pro	Val	Pro	Asn	Gln	Pro	Ile	Tyr	Ala	Leu	Gln		
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Glu	Ala	Phe	Thr	Gly	Ser	Thr	Trp	Gln	Glu	Lys	Val	Ser	Gly	Val	Arg		
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Ala	Leu	Glu	Glu	Thr	Ala	Trp	Leu	Phe	Asn	Leu	Arg	Ala	Ser	Asp	Ile		
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Pro	Tyr	Asn	Pro	Phe	Phe	Tyr	Ser	Tyr	Thr	Leu	Leu	Thr	Asp	Ser	Ser		
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Tyr	Leu	Asn	Ser	Ser	Cys	Thr	Gly	Pro	Met	Cys	Val	Gln	Ile	Glu	Asp		
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Tyr	Ser	Gln	Val	Arg	Asp	Ser	Ile	Gln	Ala	Tyr	Ser	Leu	Gly	Asp	Val		
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Arg	Ile	Trp	Ile	Gly	Thr	Ser	Tyr	Thr	Met	Tyr	Gly	Ile	Tyr	Glu	Met		
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Ile	Pro	Arg	Glu	Lys	Leu	Val	Thr	Asp	Thr	Tyr	Ser	Pro	Val	Met	Met		
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Thr	Lys	Ala	Val	Lys	Asn	Ser	Lys	Glu	Gln	Ala	Leu	Leu	Lys	Ala	Ser		
		355					360					365					
His	Val	Arg	Asp	Ala	Val	Ala	Val	Ile	Arg	Tyr	Leu	Val	Trp	Leu	Glu		
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Lys	Asn	Val	Pro	Lys	Gly	Thr	Val	Asp	Glu	Phe	Ser	Gly	Ala	Glu	Ile		
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Val	Asp	Lys	Phe	Arg	Gly	Glu	Glu	Gln	Phe	Ser	Ser	Gly	Pro	Ser	Phe		
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Glu Thr Ile Ser Ala Ser Gly Leu Asn Ala Ala Leu Ala His Tyr Ser  
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 Pro Thr Lys Glu Leu Asn Arg Lys Leu Ser Ser Asp Glu Met Tyr Leu  
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 Leu Asp Ser Gly Gly Gln Tyr Trp Asp Gly Thr Thr Asp Ile Thr Arg  
 450 455 460  
 Thr Val His Trp Gly Thr Pro Ser Ala Phe Gln Lys Glu Ala Tyr Thr  
 465 470 475 480  
 Arg Val Leu Ile Gly Asn Ile Asp Leu Ser Arg Leu Ile Phe Pro Ala  
 485 490 495  
 Ala Thr Ser Gly Arg Met Val Glu Ala Phe Ala Arg Arg Ala Leu Trp  
 500 505 510  
 Asp Ala Gly Leu Asn Tyr Gly His Gly Thr Gly His Gly Ile Gly Asn  
 515 520 525  
 Phe Leu Cys Val His Glu Trp Pro Val Gly Phe Gln Ser Asn Asn Ile  
 530 535 540  
 Ala Met Ala Lys Gly Met Phe Thr Ser Ile Glu Pro Gly Tyr Tyr Lys  
 545 550 555 560  
 Asp Gly Glu Phe Gly Ile Arg Leu Glu Asp Val Ala Leu Val Val Glu  
 565 570 575  
 Ala Lys Thr Lys Tyr Pro Gly Glu Leu Pro Asp Leu Val Val Ser Phe  
 580 585 590  
 Val Pro Tyr Asp Arg Asn Leu Ile Asp Val Ser Leu Leu Ser Pro Glu  
 595 600 605  
 His Leu Gln Tyr Leu Asn Arg Tyr Tyr Gln Thr Ile Arg Glu Lys Val  
 610 615 620  
 Gly Pro Glu Leu Gln Arg Arg Gln Leu Leu Glu Glu Phe Glu Trp Leu  
 625 630 635 640  
 Gln Gln His Thr Glu Pro Leu Ala Ala Arg Ala Pro Asp Thr Ala Ser  
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 Trp Ala Ser Val Leu Val Val Ser Thr Leu Ala Ile Leu Gly Trp Ser  
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Val

<210> 848  
 <211> 1082  
 <212> DNA  
 <213> homo sapiens



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<211> 353  
<212> PRT  
<213> homo sapiens

<400> 849  
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Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser Ile Cys  
35 40 45  
Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe Leu Leu

50

55

60

Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala  
65 70 75 80

Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn  
85 90 95

Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val  
100 105 110

Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val  
115 120 125

Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala  
130 135 140

Ser Gly Arg Gln Gln Arg Arg Arg Gln Ala Arg Val Thr Cys Val Leu  
145 150 155 160

Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg  
165 170 175

Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu  
180 185 190

Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile  
195 200 205

Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His  
210 215 220

Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val  
225 230 235 240

Gln Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val  
245 250 255

Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu  
260 265 270

Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp  
275 280 285

Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn  
290 295 300

Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg  
305 310 315 320

Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala  
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Asn

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 <211> 3733  
 <212> DNA  
 <213> homo sapiens

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 <211> 391  
 <212> PRT  
 <213> homo sapiens

<400> 851

Met	Phe	Ser	Pro	Trp	Lys	Ile	Ser	Met	Phe	Leu	Ser	Val	Arg	Glu	Ala	1	5	10	15
Ser	Val	Pro	Thr	Thr	Ala	Ser	Phe	Ser	Ala	Asp	Met	Leu	Asn	Val	Thr	20	25	30	
Leu	Gln	Gly	Pro	Thr	Leu	Asn	Gly	Thr	Phe	Ala	Gln	Ser	Lys	Cys	Pro	35	40	45	
Gln	Val	Glu	Trp	Leu	Gly	Trp	Leu	Asn	Thr	Ile	Gln	Pro	Pro	Phe	Leu	50	55	60	
Trp	Val	Leu	Phe	Val	Leu	Ala	Thr	Leu	Glu	Asn	Ile	Phe	Val	Leu	Ser	65	70	75	80
Val	Phe	Cys	Leu	His	Lys	Ser	Ser	Cys	Thr	Val	Ala	Glu	Ile	Tyr	Leu	85	90	95	
Gly	Asn	Leu	Ala	Ala	Ala	Asp	Leu	Ile	Leu	Ala	Cys	Gly	Leu	Pro	Phe	100	105	110	
Trp	Ala	Ile	Thr	Ile	Ser	Asn	Asn	Phe	Asp	Trp	Leu	Phe	Gly	Glu	Thr	115	120	125	
Leu	Cys	Arg	Val	Val	Asn	Ala	Ile	Ile	Ser	Met	Asn	Leu	Tyr	Ser	Ser	130	135	140	
Ile	Cys	Phe	Leu	Met	Leu	Val	Ser	Ile	Asp	Arg	Tyr	Leu	Ala	Leu	Val	145	150	155	160

Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys Leu  
 165 170 175  
 Tyr Ser Leu Val Ile Trp Gly Cys Thr Leu Leu Leu Ser Ser Pro Met  
 180 185 190  
 Leu Val Phe Arg Thr Met Lys Glu Tyr Ser Asp Glu Gly His Asn Val  
 195 200 205  
 Thr Ala Cys Val Ile Ser Tyr Pro Ser Leu Ile Trp Glu Val Phe Thr  
 210 215 220  
 Asn Met Leu Leu Asn Val Val Gly Phe Leu Leu Pro Leu Ser Val Ile  
 225 230 235 240  
 Thr Phe Cys Thr Met Gln Ile Met Gln Val Leu Arg Asn Asn Glu Met  
 245 250 255  
 Gln Lys Phe Lys Glu Ile Gln Thr Glu Arg Arg Ala Thr Val Leu Val  
 260 265 270  
 Leu Val Val Leu Leu Leu Phe Ile Ile Cys Trp Leu Pro Phe Gln Ile  
 275 280 285  
 Ser Thr Phe Leu Asp Thr Leu His Arg Leu Gly Ile Leu Ser Ser Cys  
 290 295 300  
 Gln Asp Glu Arg Ile Ile Asp Val Ile Thr Gln Ile Ala Ser Phe Met  
 305 310 315 320  
 Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val Tyr Val Ile Val Gly  
 325 330 335  
 Lys Arg Phe Arg Lys Lys Ser Trp Glu Val Tyr Gln Gly Val Cys Gln  
 340 345 350  
 Lys Gly Gly Cys Arg Ser Glu Pro Ile Gln Met Glu Asn Ser Met Gly  
 355 360 365  
 Thr Leu Arg Thr Ser Ile Ser Val Glu Arg Gln Ile His Lys Leu Gln  
 370 375 380  
 Asp Trp Ala Gly Ser Arg Gln  
 385 390

<210> 852  
 <211> 1284  
 <212> DNA  
 <213> homo sapiens

<400> 852  
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 cagctgcacg ttgagcatga tgggtgagagt tgcagtaaca gctccacca gcagattctg 120  
 gagacaggtg agggctcccc cagcctcaag atagcccctg ccaatgctga ctttgccttc 180

cgcttctact acctgatcgc ttcggagacc ccggggaaga acatcttttt ctccccgctg 240  
 agcatctcgg cggcctacgc catgctttcc ctgggggcct gctcacacag ccgcagccag 300  
 atccttgagg gcctgggctt caacctcacc gagctgtctg agtccgatgt ccataggggc 360  
 ttccagcacc tcctgcacac tctcaacctc cccggccatg ggctggaaac acgcgtgggc 420  
 agtgctctgt tcctgagcca caacctgaag ttccttgcaa aattcctgaa tgacaccatg 480  
 gccgtctatg aggctaaact cttccacacc aatttctacg acactgtggg cacaatccag 540  
 cttatcaacg accacgtcaa gaaggaaact cgagggaaga ttgtggattt ggtcagttag 600  
 ctcaagaagg acgtcttgat ggtgctgggt aattacattt acttcaaagc cctgtgggag 660  
 aaaccattca tttcctcaag gaccactccc aaagacttct atgttgatga gaacacaaca 720  
 gtccgggtgc ccatgatgct gcaggaccag gagcatcact ggtatcttca tgacagatac 780  
 ttgccctgct cggtgctacg gatggattac aaaggagacg caaccgtgtt tttcattctc 840  
 cctaaccaag gcaaaatgag ggagattgaa gaggttctga ctccagagat gctaattagg 900  
 tggaacaact tgttgcgga gaggaatttt tacaagaagc tagagttgca tcttcccaag 960  
 ttctccattt ctggctccta tgtattagat cagattttgc ccaggctggg cttcacggat 1020  
 ctgttctcca agtgggctga cttatccggc atcaccaaac agcaaaaact ggaggcatcc 1080  
 aaaagtttcc acaaggccac cttggacgtg gatgaggctg gcaccgaggc tgcagcagcc 1140  
 acgacgttcg cgatcaaatt cttctctgcc cagaccaatc gccacatcct gcgattcaac 1200  
 cggcccttcc ttgtgggtgat cttttccacc agcaccacga gtgtcctctt tctgggcaag 1260  
 gtcgtcgacc ccacgaaacc atag 1284

<210> 853  
 <211> 427  
 <212> PRT  
 <213> homo sapiens

<400> 853

Met His Leu Ile Asp Tyr Leu Leu Leu Leu Val Gly Leu Leu Ala  
 1 5 10 15

Leu Ser His Gly Gln Leu His Val Glu His Asp Gly Glu Ser Cys Ser  
 20 25 30

Asn Ser Ser His Gln Gln Ile Leu Glu Thr Gly Glu Gly Ser Pro Ser  
 35 40 45

Leu Lys Ile Ala Pro Ala Asn Ala Asp Phe Ala Phe Arg Phe Tyr Tyr





355

360

365

Asp Val Asp Glu Ala Gly Thr Glu Ala Ala Ala Ala Thr Thr Phe Ala  
370 375 380

Ile Lys Phe Phe Ser Ala Gln Thr Asn Arg His Ile Leu Arg Phe Asn  
385 390 395 400

Arg Pro Phe Leu Val Val Ile Phe Ser Thr Ser Thr Gln Ser Val Leu  
405 410 415

Phe Leu Gly Lys Val Val Asp Pro Thr Lys Pro  
420 425

&lt;210&gt; 854

&lt;211&gt; 1284

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;400&gt; 854

atgcatctta tcgactacct gctcctcctg ctggttgac tactggccct ttctcatggc 60  
cagctgcacg ttgagcatga tggtagaggt tgcagtaaca gctcccacca gcagattctg 120  
gagacaggtg agggctcccc cagcctcaag atagcccctg ccaatgctga ctttgccctc 180  
cgcttctact acctgatcgc ttcggagacc ccggggaaga acatcttttt ctccccgctg 240  
agcatctcgg cggcctacgc catgctttcc ctgggggcct gctcacacag ccgcagccag 300  
atccttgagg gcctgggctt caacctcacc gagctgtctg agtccgatgt ccataggggc 360  
ttccagcacc tcctgcacac tctcaacctc cccggccatg ggctggaaac atgcgtgggc 420  
agtgtctgt tcctgagcca caacctgaag ttccttgcaa aattcctgaa tgacaccatg 480  
gccgtctatg aggctaaact cttccacacc aacttctacg acactgtggg cacaatccag 540  
cttatcaacg accacgtcaa gaaggaaact cgagggaaga ttgtggattt ggtcagttag 600  
ctcaagaagg acgtcttgat ggtgctgggt aattacattt acttcaaagc cctgtgggag 660  
aaaccattca tttcctcaag gaccactccc aaagacttct atgttgatga gaacacaaca 720  
gtccgggtgc ccatgatgct gcaggaccag gagcatcact ggtatcttca tgacagatac 780  
ttgccctgct cgggtgctacg gatggattac aaaggagacg caaccgtgtt tttcattctc 840  
cctaaccaag gcaaaatgag ggagattgaa gaggttctga ctccagagat gctaattgagg 900  
tggaacaact tggtgcggaa gaggaatttt tacaagaagc tagagttgca tcttcccaag 960  
ttctccattt ctggctccta tgtattagat cagattttgc ccaggctggg cttcacggat 1020  
ctgttctcca agtgggctga cttatccggc atcaccaaac agcaaaaact ggaggcatcc 1080  
aaaagtttcc acaaggccac cttggacgtg gatgaggctg gcaccgaggc tgcagcagcc 1140

accacgttcg cgatcaaatt cttctctgcc cagaccaatc gccacatcct gcgattcaac 1200  
 cggcccttcc ttgtggtgat cttttccacc agcaccacaga gtgtcctctt tctgggcaag 1260  
 gtcgtcgacc ccacgaaacc atag 1284

<210> 855  
 <211> 427  
 <212> PRT  
 <213> homo sapiens

<400> 855

Met His Leu Ile Asp Tyr Leu Leu Leu Leu Leu Val Gly Leu Leu Ala  
 1 5 10 15  
 Leu Ser His Gly Gln Leu His Val Glu His Asp Gly Glu Ser Cys Ser  
 20 25 30  
 Asn Ser Ser His Gln Gln Ile Leu Glu Thr Gly Glu Gly Ser Pro Ser  
 35 40 45  
 Leu Lys Ile Ala Pro Ala Asn Ala Asp Phe Ala Phe Arg Phe Tyr Tyr  
 50 55 60  
 Leu Ile Ala Ser Glu Thr Pro Gly Lys Asn Ile Phe Phe Ser Pro Leu  
 65 70 75 80  
 Ser Ile Ser Ala Ala Tyr Ala Met Leu Ser Leu Gly Ala Cys Ser His  
 85 90 95  
 Ser Arg Ser Gln Ile Leu Glu Gly Leu Gly Phe Asn Leu Thr Glu Leu  
 100 105 110  
 Ser Glu Ser Asp Val His Arg Gly Phe Gln His Leu Leu His Thr Leu  
 115 120 125  
 Asn Leu Pro Gly His Gly Leu Glu Thr Cys Val Gly Ser Ala Leu Phe  
 130 135 140  
 Leu Ser His Asn Leu Lys Phe Leu Ala Lys Phe Leu Asn Asp Thr Met  
 145 150 155 160  
 Ala Val Tyr Glu Ala Lys Leu Phe His Thr Asn Phe Tyr Asp Thr Val  
 165 170 175  
 Gly Thr Ile Gln Leu Ile Asn Asp His Val Lys Lys Glu Thr Arg Gly  
 180 185 190  
 Lys Ile Val Asp Leu Val Ser Glu Leu Lys Lys Asp Val Leu Met Val  
 195 200 205  
 Leu Val Asn Tyr Ile Tyr Phe Lys Ala Leu Trp Glu Lys Pro Phe Ile  
 210 215 220

Ser Ser Arg Thr Thr Pro Lys Asp Phe Tyr Val Asp Glu Asn Thr Thr  
 225 230 235 240  
 Val Arg Val Pro Met Met Leu Gln Asp Gln Glu His His Trp Tyr Leu  
 245 250 255  
 His Asp Arg Tyr Leu Pro Cys Ser Val Leu Arg Met Asp Tyr Lys Gly  
 260 265 270  
 Asp Ala Thr Val Phe Phe Ile Leu Pro Asn Gln Gly Lys Met Arg Glu  
 275 280 285  
 Ile Glu Glu Val Leu Thr Pro Glu Met Leu Met Arg Trp Asn Asn Leu  
 290 295 300  
 Leu Arg Lys Arg Asn Phe Tyr Lys Lys Leu Glu Leu His Leu Pro Lys  
 305 310 315 320  
 Phe Ser Ile Ser Gly Ser Tyr Val Leu Asp Gln Ile Leu Pro Arg Leu  
 325 330 335  
 Gly Phe Thr Asp Leu Phe Ser Lys Trp Ala Asp Leu Ser Gly Ile Thr  
 340 345 350  
 Lys Gln Gln Lys Leu Glu Ala Ser Lys Ser Phe His Lys Ala Thr Leu  
 355 360 365  
 Asp Val Asp Glu Ala Gly Thr Glu Ala Ala Ala Thr Thr Phe Ala  
 370 375 380  
 Ile Lys Phe Phe Ser Ala Gln Thr Asn Arg His Ile Leu Arg Phe Asn  
 385 390 395 400  
 Arg Pro Phe Leu Val Val Ile Phe Ser Thr Ser Thr Gln Ser Val Leu  
 405 410 415  
 Phe Leu Gly Lys Val Val Asp Pro Thr Lys Pro  
 420 425

<210> 856  
 <211> 3428  
 <212> DNA  
 <213> homo sapiens

<220>  
 <221> misc\_feature  
 <222> (711)..(711)  
 <223> wherein N is either an "T" or a "C".

<220>  
 <221> misc\_feature  
 <222> (2085)..(2085)  
 <223> wherein N is either an "C" or a "G".

<400> 856

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tgcccaccct	ggctcccaaa	accctccaaa	acaaaagacc	agaaaagcac	tctccacca	120
gcagccaaac	gcctccttct	tgacgccagc	ccccaccctc	tgtctgctcg	agcccaggaa	180
aggcctgaag	gaacaggccg	gggaaggagc	cctccctctc	tcccttgctc	ctccatccac	240
ccagcgccgg	catctggaga	ccctatggcc	cgggctcact	ggggctgctg	cccctggctg	300
gtcctcctct	gtgcttgctg	ctggggccac	acaaagccac	tggaccttgg	agggcaggat	360
gtgagaaatt	gttccaccaa	cccccttac	cttcagtta	ctgtggtcaa	taccacaatg	420
tcactcacag	ccctccgcca	gcagatgcag	accagaatc	tctcagccta	catcatccca	480
ggcacagatg	ctcacatgaa	cgagtacatc	ggccaacatg	acgagaggcg	tgcgtggatt	540
acaggcttta	caggggtctg	aggaactgca	gtggtgacta	tgaagaaagc	agctgtctgg	600
accgacagtc	gctactggac	tcaggctgag	cggcaaatgg	actgtaattg	ggagctccat	660
aaggaagtgt	gcaccactcc	tattgtcacc	tggctcctca	ccgagattcc	ngctggaggg	720
cgtgtgggtt	ttgaccctt	cctcttgctc	attgacacct	gggagagtta	tgatctggcc	780
ctccaaggct	ctaacagaca	gctggtgtcc	atcacaacca	atcttggtga	cctggtatgg	840
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gggagcactt	ggcaggagaa	agtatctggc	gtccgaagcc	agatgcagaa	gcatcaaaag	960
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atctttcccg	ctgctacatc	agggcgaatg	gtggaggcct	ttgcccgcag	agccttgtgg	1800
gatgctggtc	tcaattatgg	tcatgggaca	ggccacggca	ttggcaactt	cctgtgtgtg	1860
catgagtggc	cagtgggatt	ccagtccaac	aacatcgcta	tggccaaggg	catgttcact	1920
tccattgaac	ctggttacta	taaggatgga	gaatttggga	tccgtctcga	agatgtggct	1980
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caaagtgcag	ccacagctac	aatgctgtta	aatcctccca	catttcttgg	atgccccttc	3120
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gccctctcct	cattctctga	accactgtg	gtgagaagaa	tttgctccgg	ccaaattggc	3360
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gcctgtgg

3428

<210> 857  
<211> 673  
<212> PRT  
<213> homo sapiens

<400> 857

Met Ala Arg Ala His Trp Gly Cys Cys Pro Trp Leu Val Leu Leu Cys  
1 5 10 15  
Ala Cys Ala Trp Gly His Thr Lys Pro Leu Asp Leu Gly Gly Gln Asp  
20 25 30  
Val Arg Asn Cys Ser Thr Asn Pro Pro Tyr Leu Pro Val Thr Val Val  
35 40 45  
Asn Thr Thr Met Ser Leu Thr Ala Leu Arg Gln Gln Met Gln Thr Gln  
50 55 60  
Asn Leu Ser Ala Tyr Ile Ile Pro Gly Thr Asp Ala His Met Asn Glu  
65 70 75 80  
Tyr Ile Gly Gln His Asp Glu Arg Arg Ala Trp Ile Thr Gly Phe Thr  
85 90 95  
Gly Ser Ala Gly Thr Ala Val Val Thr Met Lys Lys Ala Ala Val Trp  
100 105 110  
Thr Asp Ser Arg Tyr Trp Thr Gln Ala Glu Arg Gln Met Asp Cys Asn  
115 120 125  
Trp Glu Leu His Lys Glu Val Gly Thr Thr Pro Ile Val Thr Trp Leu  
130 135 140  
Leu Thr Glu Ile Pro Ala Gly Gly Arg Val Gly Phe Asp Pro Phe Leu  
145 150 155 160  
Leu Ser Ile Asp Thr Trp Glu Ser Tyr Asp Leu Ala Leu Gln Gly Ser  
165 170 175  
Asn Arg Gln Leu Val Ser Ile Thr Thr Asn Leu Val Asp Leu Val Trp  
180 185 190  
Gly Ser Glu Arg Pro Pro Val Pro Asn Gln Pro Ile Tyr Ala Leu Gln  
195 200 205  
Glu Ala Phe Thr Gly Ser Thr Trp Gln Glu Lys Val Ser Gly Val Arg  
210 215 220  
Ser Gln Met Gln Lys His Gln Lys Val Pro Thr Ala Val Leu Leu Ser  
225 230 235 240  
Ala Leu Glu Glu Thr Ala Trp Leu Phe Asn Leu Arg Ala Ser Asp Ile  
245 250 255

Pro Tyr Asn Pro Phe Phe Tyr Ser Tyr Thr Leu Leu Thr Asp Ser Ser  
 260 265 270  
 Ile Arg Leu Phe Ala Asn Lys Ser Arg Phe Ser Ser Glu Thr Leu Ser  
 275 280 285  
 Tyr Leu Asn Ser Ser Cys Thr Gly Pro Met Cys Val Gln Ile Glu Asp  
 290 295 300  
 Tyr Ser Gln Val Arg Asp Ser Ile Gln Ala Tyr Ser Leu Gly Asp Val  
 305 310 315 320  
 Arg Ile Trp Ile Gly Thr Ser Tyr Thr Met Tyr Gly Ile Tyr Glu Met  
 325 330 335  
 Ile Pro Arg Glu Lys Leu Val Thr Asp Thr Tyr Ser Pro Val Met Met  
 340 345 350  
 Thr Lys Ala Val Lys Asn Ser Lys Glu Gln Ala Leu Leu Lys Ala Ser  
 355 360 365  
 His Val Arg Asp Ala Val Ala Val Ile Arg Tyr Leu Val Trp Leu Glu  
 370 375 380  
 Lys Asn Val Pro Lys Gly Thr Val Asp Glu Phe Ser Gly Ala Glu Ile  
 385 390 395 400  
 Val Asp Lys Phe Arg Gly Glu Glu Gln Phe Ser Ser Gly Pro Ser Phe  
 405 410 415  
 Glu Thr Ile Ser Ala Ser Gly Leu Asn Ala Ala Leu Ala His Tyr Ser  
 420 425 430  
 Pro Thr Lys Glu Leu Asn Arg Lys Leu Ser Ser Asp Glu Met Tyr Leu  
 435 440 445  
 Leu Asp Ser Gly Gly Gln Tyr Trp Asp Gly Thr Thr Asp Ile Thr Arg  
 450 455 460  
 Thr Val His Trp Gly Thr Pro Ser Ala Phe Gln Lys Glu Ala Tyr Thr  
 465 470 475 480  
 Arg Val Leu Ile Gly Asn Ile Asp Leu Ser Arg Leu Ile Phe Pro Ala  
 485 490 495  
 Ala Thr Ser Gly Arg Met Val Glu Ala Phe Ala Arg Arg Ala Leu Trp  
 500 505 510  
 Asp Ala Gly Leu Asn Tyr Gly His Gly Thr Gly His Gly Ile Gly Asn  
 515 520 525  
 Phe Leu Cys Val His Glu Trp Pro Val Gly Phe Gln Ser Asn Asn Ile  
 530 535 540  
 Ala Met Ala Lys Gly Met Phe Thr Ser Ile Glu Pro Gly Tyr Tyr Lys  
 545 550 555 560

Asp Gly Glu Phe Gly Ile Arg Leu Glu Asp Val Ala Leu Val Val Glu  
565 570 575

Ala Lys Thr Lys Tyr Pro Gly Glu Leu Pro Asp Leu Val Val Ser Phe  
580 585 590

Val Pro Tyr Asp Arg Asn Leu Ile Asp Val Ser Leu Leu Ser Pro Glu  
595 600 605

His Leu Gln Tyr Leu Asn Arg Tyr Tyr Gln Thr Ile Arg Glu Lys Val  
610 615 620

Gly Pro Glu Leu Gln Arg Arg Gln Leu Leu Glu Glu Phe Glu Trp Leu  
625 630 635 640

Gln Gln His Thr Glu Pro Leu Ala Ala Arg Ala Pro Asp Thr Ala Ser  
645 650 655

Trp Ala Ser Val Leu Val Val Ser Thr Leu Ala Ile Leu Gly Trp Ser  
660 665 670

Val

<210> 858  
<211> 19  
<212> DNA  
<213> homo sapiens

<400> 858  
gagccgggta aggtctggt

19

<210> 859  
<211> 19  
<212> DNA  
<213> homo sapiens

<400> 859  
gctaggggct tcggacctt

19

<210> 860  
<211> 19  
<212> DNA  
<213> homo sapiens

<400> 860  
aacaggatgt cccaacagg

19

<210> 861  
<211> 19  
<212> DNA  
<213> homo sapiens



<400> 861  
tccaggaact gagtgccaa

19

<210> 862  
<211> 19  
<212> DNA  
<213> homo sapiens

<400> 862  
catggtccca ggagagccc

19

<210> 863  
<211> 17  
<212> DNA  
<213> homo sapiens

<400> 863  
cctgttgggc atagcca

17

<210> 864  
<211> 19  
<212> DNA  
<213> homo sapiens

<400> 864  
ccctccagca ggaatctcg

19

<210> 865  
<211> 19  
<212> DNA  
<213> homo sapiens

<400> 865  
acaaggtgca ggggccgca

19

<210> 866  
<211> 19  
<212> DNA  
<213> homo sapiens

<400> 866  
gtgggccctg tataatcac

19

<210> 867  
<211> 19  
<212> DNA  
<213> homo sapiens

<400> 867  
ctcaagggtc caagtgatc

19

<210> 868  
<211> 19  
<212> DNA  
<213> homo sapiens

<400> 868  
acaagtatca ggtaatggc 19

<210> 869  
<211> 19  
<212> DNA  
<213> homo sapiens

<400> 869  
cctctcttat tacacttcc 19

<210> 870  
<211> 19  
<212> DNA  
<213> homo sapiens

<400> 870  
gttgtgaggg ttaaaggca 19

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<400> 1170  
gtcagcctta gggtaacagt tttg 24

<210> 1171  
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<210> 1173  
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<400> 1173  
gatgaagata ttggagcaag acttttag 28

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<400> 1176  
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<400> 1177  
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accccccaat ctacggga

18

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<400> 1179  
ccaccaggaa gatgctgatg

20

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<212> DNA  
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<400> 1180  
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21

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<400> 1181  
ctcacctgtg ctgcttggtg

19

<210> 1182  
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<400> 1182  
gtggcgggtg gaagcacc

18

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21

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<400> 1184  
cgggccctatg catggtgta

19

<210> 1185  
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aaaaaaaagag gctgtgtttt gtca

24

<210> 1186  
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<212> DNA  
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<400> 1186  
aaggtggccc agtatgagc

19

<210> 1187  
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<400> 1187  
cagtgatggg gaattcatta tcc

23

<210> 1188  
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<212> DNA  
<213> Homo sapiens

<400> 1188  
cataaatgcc cctcctccat

20

<210> 1189  
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<213> Homo sapiens

<400> 1189  
cattgagtca gggactcagc a

21

<210> 1190  
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<212> DNA  
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<400> 1190  
cactctgagt ccaaattgttc tctc

24

<210> 1191  
<211> 19  
<212> DNA  
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<400> 1191  
ctcacctgtg ctgcttgtg 19

<210> 1192  
<211> 20  
<212> DNA  
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<400> 1192  
ctcttcccca gatccactgg 20

<210> 1193  
<211> 21  
<212> DNA  
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<400> 1193  
catacatctc cgaagaaacg g 21

<210> 1194  
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gcaggagtgc agagctcag 19

<210> 1195  
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<400> 1195  
gttctccgtc cctgcccc 18

<210> 1196  
<211> 22  
<212> DNA  
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<400> 1196  
gaaagagaag gagccatctc ca 22

<210> 1197  
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<212> DNA  
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<400> 1197  
caaccctgca ctccaagc

18

<210> 1198  
<211> 21  
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<400> 1198  
gtttgggacc ccatgttcta t

21

<210> 1199  
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<212> DNA  
<213> Homo sapiens

<400> 1199  
gtacatgtga ggcacwtta cgc

23

<210> 1200  
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<212> DNA  
<213> Homo sapiens

<400> 1200  
catcttgaag gaactcaaag actca

25

<210> 1201  
<211> 23  
<212> DNA  
<213> Homo sapiens

<400> 1201  
ctttggatga aaaagaggaa gca

23

<210> 1202  
<211> 21  
<212> DNA  
<213> Homo sapiens

<400> 1202  
caagagaagg cgtcttttga t

21

<210> 1203  
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<400> 1203  
caaagaggcc ctgcccga 18

<210> 1204  
<211> 18  
<212> DNA  
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<400> 1204  
aacccttac ccaccagc 18

<210> 1205  
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<212> DNA  
<213> Homo sapiens

<400> 1205  
ggagaccaag gttccagctc 20

<210> 1206  
<211> 23  
<212> DNA  
<213> Homo sapiens

<400> 1206  
gaagtcgttg tgagggttaa agg 23

<210> 1207  
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<212> DNA  
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<400> 1207  
aggtcttcac ctgctctgca 20

<210> 1208  
<211> 22  
<212> DNA  
<213> Homo sapiens

<400> 1208  
caaactcaga ttgtgggaga gc 22

<210> 1209  
<211> 19  
<212> DNA  
<213> Homo sapiens

<400> 1209  
ttgagttggt tgcggcaa 19

<210> 1210  
<211> 20  
<212> DNA  
<213> Homo sapiens

<400> 1210  
gatgctgaat ggggaaaagg 20

<210> 1211  
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<212> DNA  
<213> Homo sapiens

<400> 1211  
catatactcg ccccatgaag ac 22

<210> 1212  
<211> 21  
<212> DNA  
<213> Homo sapiens  
  
<400> 1212  
cacaacgaat ggtactacgg c 21

<210> 1213  
<211> 20  
<212> DNA  
<213> Homo sapiens  
  
<400> 1213  
catcatacat cccctccagc 20

<210> 1214  
<211> 20  
<212> DNA  
<213> Homo sapiens  
  
<400> 1214  
ctaccacgag caagtctctg 20

<210> 1215  
<211> 24  
<212> DNA  
<213> Homo sapiens  
  
<400> 1215  
ctgktgact caaaccaat cact 24

<210> 1216  
<211> 27



<212> DNA  
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<400> 1216  
tcaaaaaatc tcaattcttc cctatct

27

<210> 1217  
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<212> DNA  
<213> Homo sapiens

<400> 1217  
catggaaatt cccttcatct g

21

<210> 1218  
<211> 18  
<212> DNA  
<213> Homo sapiens

<400> 1218  
cccacgagga ggagccag

18

<210> 1219  
<211> 23  
<212> DNA  
<213> Homo sapiens

<400> 1219  
acacacagca tgaagtctgt cac

23

<210> 1220  
<211> 18  
<212> DNA  
<213> Homo sapiens

<400> 1220  
cttccctggc cttttctc

18

<210> 1221  
<211> 23  
<212> DNA  
<213> Homo sapiens

<400> 1221  
catacaattc tctggttcga tgc

23

<210> 1222  
<211> 18  
<212> DNA  
<213> Homo sapiens

<400> 1222  
gggagaaaaa gggctgca 18

<210> 1223  
<211> 18  
<212> DNA  
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<400> 1223  
cctttcccca cctgctgg 18

<210> 1224  
<211> 18  
<212> DNA  
<213> Homo sapiens

<400> 1224  
cagcctcagc cgagtggg 18

<210> 1225  
<211> 27  
<212> DNA  
<213> Homo sapiens

<400> 1225  
gaattgatta tttttgagtg cacagtc 27

<210> 1226  
<211> 24  
<212> DNA  
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<400> 1226  
gcaaatttag ccaagtcaaa gaga 24

<210> 1227  
<211> 24  
<212> DNA  
<213> Homo sapiens

<400> 1227  
gctgaaagac cagaacaaga attc 24

<210> 1228  
<211> 26  
<212> DNA  
<213> Homo sapiens

<400> 1228  
tggaagagtt tgtaaccag ataatc 26

<210> 1229  
<211> 24  
<212> DNA  
<213> Homo sapiens

<400> 1229  
acatggcaaa gaagtaaatt gctg

24

<210> 1230  
<211> 31  
<212> DNA  
<213> Homo sapiens

<400> 1230  
gttaccaaata acaacaacaa taaccagtat t

31

<210> 1231  
<211> 27  
<212> DNA  
<213> Homo sapiens

<400> 1231  
tttgaaacca agaattctcct ttaattt

27

<210> 1232  
<211> 18  
<212> DNA  
<213> Homo sapiens

<400> 1232  
tgcctccctg ctcatttg

18

<210> 1233  
<211> 18  
<212> DNA  
<213> Homo sapiens

<400> 1233  
atgtggcgat tggctctgg

18

<210> 1234  
<211> 23  
<212> DNA  
<213> Homo sapiens

<400> 1234  
catggtgtca ttcaggaatt ttg

23

<210> 1235  
<211> 28

<212> DNA  
<213> Homo sapiens

<400> 1235  
cagtagaact ggtctttgta ttgttacc 28

<210> 1236  
<211> 18  
<212> DNA  
<213> Homo sapiens

<400> 1236  
gcagcatcat gggcaccc 18

<210> 1237  
<211> 28  
<212> DNA  
<213> Homo sapiens

<400> 1237  
gatgcaactc tagcttcttg taaaaatt 28

<210> 1238  
<211> 29  
<212> DNA  
<213> Homo sapiens

<400> 1238  
gatttagcat ataccaatga tctgactct 29

<210> 1239  
<211> 27  
<212> DNA  
<213> Homo sapiens

<400> 1239  
tttcagatga gttgatttca ttagtgc 27

<210> 1240  
<211> 27  
<212> DNA  
<213> Homo sapiens

<400> 1240  
cacttgtctt tcagatgagt tgatttc 27

<210> 1241  
<211> 28  
<212> DNA  
<213> Homo sapiens

<400> 1241  
ctgtagagggt cagtagaact ggtctttg 28

<210> 1242  
<211> 27  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> misc\_feature  
<222> (14)..(14)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1242  
cctcatcgat gtengcctgc tgtctcc 27

<210> 1243  
<211> 25  
<212> DNA  
<213> Homo sapiens

<400> 1243  
gtggtttgca aaccttagca tgcac 25

<210> 1244  
<211> 22  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (12)..(12)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1244  
tggaagccca gnccccagag gt 22

<210> 1245  
<211> 25  
<212> DNA  
<213> Homo sapiens

<400> 1245  
agcccaggcc ccagaggtgc tccca 25

<210> 1246  
<211> 27  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (12)..(12)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>  
<221> misc\_feature  
<222> (14)..(14)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1246  
aatgttgaga angncagcct aaccctg

27

<210> 1247  
<211> 27  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (18)..(18)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>  
<221> misc\_feature  
<222> (21)..(21)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1247  
cccggsetct tccttcangc ntttct

27

<210> 1248  
<211> 27  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (12)..(12)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1248  
agaaaagctt gnctcaggca gatcagc

27

<210> 1249  
<211> 25  
<212> DNA  
<213> Homo sapiens

<400> 1249  
tacctaaata aataataaaa gccag 25

<210> 1250  
<211> 27  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> misc\_feature  
<222> (17)..(17)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1250  
gcaacaagtc tcctttncag aacagtc 27

<210> 1251  
<211> 27  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> misc\_feature  
<222> (19)..(19)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1251  
agacttcacc tcttggcanc ttggctt 27

<210> 1252  
<211> 25  
<212> DNA  
<213> Homo sapiens

<400> 1252  
ctgcatgttg ctgaagggtg aaaga 25

<210> 1253  
<211> 27  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> misc\_feature  
<222> (3)..(3)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>  
<221> misc\_feature  
<222> (16)..(16)

<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1253

ttngagcctg tggctncaac cagacct

27

<210> 1254

<211> 27

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (9)..(9)

<223> wherein "n" equals a C3 phosphoramidite linker.

<220>

<221> misc\_feature

<222> (19)..(19)

<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1254

ttaccctang gctgacctnc caggaac

27

<210> 1255

<211> 25

<212> DNA

<213> Homo sapiens

<400> 1255

tcacctggct cctcaccgag attcc

25

<210> 1256

<211> 27

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (9)..(9)

<223> wherein "n" equals a C3 phosphoramidite linker.

<220>

<221> misc\_feature

<222> (19)..(19)

<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1256

tatttcagnc cactgacang gcctcag

27



<210> 1257  
<211> 25  
<212> DNA  
<213> Homo sapiens

<400> 1257  
accttcataag aggtataat aaaag

25

<210> 1258  
<211> 25  
<212> DNA  
<213> Homo sapiens

<400> 1258  
aagagtttgt ttgaggaaag gggttt

25

<210> 1259  
<211> 27  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (15)..(15)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>  
<221> misc\_feature  
<222> (18)..(18)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1259  
gtaaaggagg tctcnatngc acagggg

27

<210> 1260  
<211> 27  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (15)..(15)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1260  
cacagagtag agagnattgc cacgaaa

27

<210> 1261  
<211> 25

<212> DNA  
 <213> Homo sapiens  
 <400> 1261  
 ccagtaattt atgtctttgt gggcc

25

<210> 1262  
 <211> 25  
 <212> DNA  
 <213> Homo sapiens  
 <400> 1262  
 atcctgaatt atccaagtgg gccct

25

<210> 1263  
 <211> 25  
 <212> DNA  
 <213> Homo sapiens  
 <400> 1263  
 cagcaggaaa caaataacaa gtatc

25

<210> 1264  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (18)..(18)  
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1264  
 acaagtatcr ggtaatgncc tctctta

27

<210> 1265  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (14)..(14)  
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1265  
 ctgggacctg ctgnacagag tgctgcc

27

<210> 1266  
 <211> 27

<212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> misc\_feature  
 <222> (9)..(9)  
 <223> wherein "n" equals a C3 phosphoramidite linker.

<220>  
 <221> misc\_feature  
 <222> (11)..(11)  
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1266  
 tgaaccaana ngcttggtt tcttatc 27

<210> 1267  
 <211> 25  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 1267  
 gagccctcct ctgccgtgtc atcaa 25

<210> 1268  
 <211> 25  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 1268  
 agatctgaac atcaccgcct gcatc 25

<210> 1269  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> misc\_feature  
 <222> (14)..(14)  
 <223> wherein "n" equals a C3 phosphoramidite linker.

<220>  
 <221> misc\_feature  
 <222> (17)..(17)  
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1269  
 cactgggcaa atcngcnggg ctcccc 27

<210> 1270  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> misc\_feature  
 <222> (3)..(3)  
 <223> wherein "n" equals a C3 phosphoramidite linker.

<220>  
 <221> misc\_feature  
 <222> (16)..(16)  
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1270  
 gtnggaatga caggtngaag ggagcca 27

<210> 1271  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> misc\_feature  
 <222> (16)..(16)  
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1271  
 ttacaacata acagcncatt gagtctt 27

<210> 1272  
 <211> 25  
 <212> DNA  
 <213> Homo sapiens

<400> 1272  
 taacagctca ttgagtcttk cacag 25

<210> 1273  
 <211> 25  
 <212> DNA  
 <213> Homo sapiens

<400> 1273  
 gggcagtcac tcagcaccag agcac 25

<210> 1274  
 <211> 25

<212> DNA  
 <213> Homo sapiens  
 <400> 1274  
 ccctagaaga gtgtgaaaag gaatg

25

<210> 1275  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> misc\_feature  
 <222> (15)..(15)  
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1275  
 attccttcac tcatntatna aacaaaa

27

<210> 1276  
 <211> 25  
 <212> DNA  
 <213> Homo sapiens

<400> 1276  
 tacgttgagc gatgagcccc aggtt

25

<210> 1277  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (16)..(16)  
 <223> wherein "n" equals a C3 phosphoramidite linker.

<220>  
 <221> misc\_feature  
 <222> (19)..(19)  
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1277  
 acaggggctg gggatngcna aatacac

27

<210> 1278  
 <211> 22  
 <212> DNA  
 <213> Homo sapiens

<400> 1278  
gtggtgggca cggagtcctc ac 22

<210> 1279  
<211> 27  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> misc\_feature  
<222> (14)..(14)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1279  
gtcagggagg ggcncacctg ggcgcgg 27

<210> 1280  
<211> 27  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> misc\_feature  
<222> (7)..(7)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1280  
tttttgnagc cttaaaaccc ttccttc 27

<210> 1281  
<211> 25  
<212> DNA  
<213> Homo sapiens

<400> 1281  
gcagaagctg tcctgtttcc tgggt 25

<210> 1282  
<211> 27  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> misc\_feature  
<222> (19)..(19)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1282  
gaagtgccca ggaggctgnt gacatca 27

<210> 1283  
 <211> 22  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> misc\_feature  
 <222> (13)..(13)  
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1283  
 cattgcacca aanctggatg gc

22

<210> 1284  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> misc\_feature  
 <222> (7)..(7)  
 <223> wherein "n" equals a C3 phosphoramidite linker.

<220>  
 <221> misc\_feature  
 <222> (15)..(15)  
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1284  
 gcttttcnggt ggtgncagtgc cccagtc

27

<210> 1285  
 <211> 25  
 <212> DNA  
 <213> Homo sapiens

<400> 1285  
 gagcgaaggg ctggctgagg tcatg

25

<210> 1286  
 <211> 25  
 <212> DNA  
 <213> Homo sapiens

<400> 1286  
 accttttgct tgatttttca ctgta

25

<210> 1287  
 <211> 25

<212> DNA  
<213> Homo sapiens  
  
<400> 1287  
ggctcccaat actgattctg ctcca

25

<210> 1288  
<211> 27  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> misc\_feature  
<222> (18)..(18)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1288  
accacagca ccctgctnga cegtctc

27

<210> 1289  
<211> 27  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> misc\_feature  
<222> (16)..(16)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1289  
agggttcag ggaganctgg gatgagg

27

<210> 1290  
<211> 27  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> misc\_feature  
<222> (11)..(11)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1290  
gctgggatga ngcytggggt gctgcct

27

<210> 1291  
<211> 25  
<212> DNA  
<213> Homo sapiens



<400> 1291  
gttctctgga gaaaaaactg tgctg

25

<210> 1292  
<211> 27  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (17)..(17)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1292  
ccccctctcc aagtctntgt cccacaa

27

<210> 1293  
<211> 25  
<212> DNA  
<213> Homo sapiens

<400> 1293  
gaagagggaa ctgaggcagg gacag

25

<210> 1294  
<211> 27  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (15)..(15)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>  
<221> misc\_feature  
<222> (18)..(18)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1294  
aagggtgcta cgtanatntg aggcac

27

<210> 1295  
<211> 25  
<212> DNA  
<213> Homo sapiens

<400> 1295  
cccagcgctg gggaaagaaa ggaca

25

<210> 1296  
<211> 25  
<212> DNA  
<213> Homo sapiens

<400> 1296  
gagatgcggt aggaagactg ttaag

25

<210> 1297  
<211> 27  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (10)..(10)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>  
<221> misc\_feature  
<222> (15)..(15)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1297  
aagctggaan cctcnaggat gggttca

27

<210> 1298  
<211> 22  
<212> DNA  
<213> Homo sapiens

<400> 1298  
aagctctacc acgccttctc ag

22

<210> 1299  
<211> 27  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (10)..(10)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>  
<221> misc\_feature  
<222> (13)..(13)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1299  
ggaacttgtn ctntcgggtcc cagagca

27

<210> 1300  
<211> 25  
<212> DNA  
<213> Homo sapiens

<400> 1300  
tactggcgaa gacagcggcg atggg

25

<210> 1301  
<211> 22  
<212> DNA  
<213> Homo sapiens

<400> 1301  
ccagcaggag agccaggacc ca

22

<210> 1302  
<211> 22  
<212> DNA  
<213> Homo sapiens

<400> 1302  
ccaagcgcaa ggtgagcagg gg

22

<210> 1303  
<211> 22  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (12)..(12)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1303  
aggtcggacc ancttttccc aa

22

<210> 1304  
<211> 27  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (14)..(14)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>  
<221> misc\_feature  
<222> (17)..(17)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>  
<221> misc\_feature  
<222> (20)..(20)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1304  
tccctatctt tgcnacnctn atgctgt

27

<210> 1305  
<211> 27  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (19)..(19)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1305  
acccatactg acccttttng caagtcc

27

<210> 1306  
<211> 27  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (10)..(10)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>  
<221> misc\_feature  
<222> (21)..(21)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1306  
agagcagttg gaggtcaggt ncagga

27

<210> 1307  
<211> 25  
<212> DNA  
<213> Homo sapiens

<400> 1307  
caaaatcctg cctaatagtg agtgc

25

<210> 1308  
<211> 27  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (8)..(8)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1308  
tcccttgnac rcaggagtcc ccacccc

27

<210> 1309  
<211> 27  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (10)..(10)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>  
<221> misc\_feature  
<222> (14)..(14)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1309  
gctgtgaagn tcgnggagtt gccccacc

27

<210> 1310  
<211> 22  
<212> DNA  
<213> Homo sapiens

<400> 1310  
aaggcrggga tggggactcc tg

22

<210> 1311  
<211> 22  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (3)..(3)

<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1311

tgnggccacc ccagctgtgt ca

22

<210> 1312

<211> 25

<212> DNA

<213> Homo sapiens

<400> 1312

atgtgtgtca cgttctgcca tcacc

25

<210> 1313

<211> 27

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (17)..(17)

<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1313

atctggaact tatagtnttg aaaagaa

27

<210> 1314

<211> 27

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (14)..(14)

<223> wherein "n" equals a C3 phosphoramidite linker.

<220>

<221> misc\_feature

<222> (19)..(19)

<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1314

gaggggttcc agangtacnt atattta

27

<210> 1315

<211> 25

<212> DNA

<213> Homo sapiens

<400> 1315  
aagtagacaa ggaatgggtg tgaaa

25

<210> 1316  
<211> 27  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (11)..(11)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>  
<221> misc\_feature  
<222> (13)..(13)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>  
<221> misc\_feature  
<222> (15)..(15)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>  
<221> misc\_feature  
<222> (19)..(19)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1316  
tcataatcac nantnaaant tagtagc

27

<210> 1317  
<211> 25  
<212> DNA  
<213> Homo sapiens

<400> 1317  
gaaattttgc tgaagagaat gctaa

25

<210> 1318  
<211> 25  
<212> DNA  
<213> Homo sapiens

<400> 1318  
cacatgtaaa tgactcagaa taatg

25

<210> 1319  
<211> 27

<212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> misc\_feature  
 <222> (16)..(16)  
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1319  
 ttcagttcta ggaatnatat cagacac

27

<210> 1320  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> misc\_feature  
 <222> (9)..(9)  
 <223> wherein "n" equals a C3 phosphoramidite linker.

<220>  
 <221> misc\_feature  
 <222> (19)..(19)  
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1320  
 cttggtaana agcccatna attcttc

27

<210> 1321  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> misc\_feature  
 <222> (3)..(3)  
 <223> wherein "n" equals a C3 phosphoramidite linker.

<220>  
 <221> misc\_feature  
 <222> (15)..(15)  
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1321  
 ggntggcacc gaggntgcag cagccac

27

<210> 1322  
 <211> 27



<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (7)..(7)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>  
<221> misc\_feature  
<222> (12)..(12)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1322  
aacctcnccg gncatgggct ggaaaca

27

<210> 1323  
<211> 27  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (2)..(2)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>  
<221> misc\_feature  
<222> (18)..(18)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1323  
tntcttggac agatgttnat tatgaaa

27

<210> 1324  
<211> 27  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (9)..(9)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1324  
ccggactgnt gtgttctcat caacata

27

<210> 1325  
<211> 27

<212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> misc\_feature  
 <222> (17)..(17)  
 <223> wherein "n" equals a C3 phosphoramidite linker.

<220>  
 <221> misc\_feature  
 <222> (20)..(20)  
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1325  
 gatcctggct tggtcantan tctaattg 27

<210> 1326  
 <211> 25  
 <212> DNA  
 <213> Homo sapiens

<400> 1326  
 gaggaagat tgtggatttg gtcag 25

<210> 1327  
 <211> 25  
 <212> DNA  
 <213> Homo sapiens

<400> 1327  
 agaccctaaa ataaactctg aggat 25

<210> 1328  
 <211> 25  
 <212> DNA  
 <213> Homo sapiens

<400> 1328  
 taaaccatat aaagcactcc acaga 25

<210> 1329  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> wherein "n" equals a C3 phosphoramidite linker.

<220>  
<221> misc\_feature  
<222> (17)..(17)  
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1329  
tatgaaacgn gtaccanttc tatcccc 27

<210> 1330  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1330  
tgtaaaacga cggccagtag ttctctctcc tccctcact 39

<210> 1331  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1331  
tgtaaaacga cggccagtgg cattcacagg tgattcagt 39

<210> 1332  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1332  
tgtaaaacga cggccagttt ctgggcttta ccctctctc 39

<210> 1333  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1333  
tgtaaaacga cggccagttt ctgggcttta ccctctctc 39

<210> 1334  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1334  
tgtaaaacga cggccagtcc aggtgcagga ttaacagac 39

<210> 1335  
<211> 39

<212> DNA  
 <213> Homo sapiens  
  
 <400> 1335  
 tgtaaaacga cggccagtac taggaacttg cacagtccg 39  
  
 <210> 1336  
 <211> 39  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 1336  
 tgtaaaacga cggccagtcc tcacacccta tcctacacg 39  
  
 <210> 1337  
 <211> 38  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 1337  
 tgtaaaacga cggccagtca gtgagatctt gccactgc 38  
  
 <210> 1338  
 <211> 39  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 1338  
 tgtaaaacga cggccagtca ggcagacaat gatgtgatg 39  
  
 <210> 1339  
 <211> 39  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 1339  
 tgtaaaacga cggccagtta tccaggtatg gtggcatgt 39  
  
 <210> 1340  
 <211> 37  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 1340  
 tgtaaaacga cggccagtca gaggggaagca cgtgatg 37  
  
 <210> 1341  
 <211> 39  
 <212> DNA  
 <213> Homo sapiens

<400> 1341  
tgtaaaacga cggccagttg taaagccctt tgcagaagt 39

<210> 1342  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1342  
tgtaaaacga cggccagtct ctgaaaagcc ccagagaat 39

<210> 1343  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1343  
tgtaaaacga cggccagtga ggctccagac tctcctggt 39

<210> 1344  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1344  
tgtaaaacga cggccagtca ttgcctagaa acctttgca 39

<210> 1345  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1345  
tgtaaaacga cggccagtag ccacagctac aatgctggt 39

<210> 1346  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1346  
tgtaaaacga cggccagtct gccgtcaaca cagaactct 39

<210> 1347  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1347  
tgtaaaacga cggccagtag aagaacagtt ctctccgg 39

<210> 1348  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1348  
tgtaaaacga cggccagtca tgccttgccct tgtactttc

39

<210> 1349  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1349  
tgtaaaacga cggccagtat ggaacacaga ggggttagg

39

<210> 1350  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1350  
tgtaaaacga cggccagtgg gttgtatacc acaccctgg

39

<210> 1351  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1351  
tgtaaaacga cggccagtcg agataggaaa gccagctag

39

<210> 1352  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1352  
tgtaaaacga cggccagtca cttgtggaaa gcacacaga

39

<210> 1353  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1353  
tgtaaaacga cggccagtag gaaatttgag gccatcact

39

<210> 1354  
<211> 39

<212> DNA  
<213> Homo sapiens

<400> 1354  
tgtaaaacga cggccagtag cagtcaagat cccttccat 39

<210> 1355  
<211> 38  
<212> DNA  
<213> Homo sapiens

<400> 1355  
tgtaaaacga cggccagtga aagagccctc cctctctc 38

<210> 1356  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1356  
tgtaaaacga cggccagtca aggtggacag tcttcggta 39

<210> 1357  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1357  
tgtaaaacga cggccagttc ctcatagcag ccctattga 39

<210> 1358  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1358  
tgtaaaacga cggccagtat ccgaagacag ggagttcat 39

<210> 1359  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1359  
tgtaaaacga cggccagtat ccgaagacag ggagttcat 39

<210> 1360  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1360  
tgtaaaacga cggccagttc tttgccttcc tggaattct 39

<210> 1361  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1361  
tgtaaaacga cggccagtcg tcccagatct gaacatcac 39

<210> 1362  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1362  
tgtaaaacga cggccagtga accaagaagc ttggctttc 39

<210> 1363  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1363  
tgtaaaacga cggccagtaa cttcccagac tcaagggat 39

<210> 1364  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1364  
tgtaaaacga cggccagtca agtgatcctc cactttggt 39

<210> 1365  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1365  
tgtaaaacga cggccagtcc tccacttttg tctcccata 39

<210> 1366  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1366  
tgtaaaacga cggccagtgc tgtagtctgc cacttcctg 39



<210> 1367  
<211> 38  
<212> DNA  
<213> Homo sapiens

<400> 1367  
tgtaaaacga cggccagtag gaccaagggtc tgggaact 38

<210> 1368  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1368  
tgtaaaacga cggccagtgc ctggaacaca gaccattaa 39

<210> 1369  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1369  
tgtaaaacga cggccagtaa cttcccagac tcaagggat 39

<210> 1370  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1370  
tgtaaaacga cggccagtcc cttctgggca gagaatata 39

<210> 1371  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1371  
tgtaaaacga cggccagtcc cttctgggca gagaatata 39

<210> 1372  
<211> 36  
<212> DNA  
<213> Homo sapiens

<400> 1372  
tgtaaaacga cggccagtgc atcttctctgg tggtgg 36

<210> 1373  
<211> 39

<212> DNA  
<213> Homo sapiens

<400> 1373  
tgtaaaaacga cggccagtcg tcccagatct gaacatcac 39

<210> 1374  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1374  
tgtaaaaacga cggccagtgt ggtcttttaa ggaggcctg 39

<210> 1375  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1375  
tgtaaaaacga cggccagtgg tctcagcact gtgacctc 39

<210> 1376  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1376  
tgtaaaaacga cggccagttc gggagttgta acaaatgct 39

<210> 1377  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1377  
tgtaaaaacga cggccagtgc tatgcaaaaa cctcatcca 39

<210> 1378  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1378  
tgtaaaaacga cggccagtca tctacaccat gcatagggc 39

<210> 1379  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1379  
tgtaaaacga cggccagtta gcctctccag ttctagccc 39

<210> 1380  
<211> 40  
<212> DNA  
<213> Homo sapiens

<400> 1380  
tgtaaaacga cggccagtaa taaaagaggt gctgaccac 40

<210> 1381  
<211> 38  
<212> DNA  
<213> Homo sapiens

<400> 1381  
tgtaaaacga cggccagtcc accatgaccc aagtttat 38

<210> 1382  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1382  
tgtaaaacga cggccagtga ggaatccctt tgactcacc 39

<210> 1383  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1383  
tgtaaaacga cggccagttg gttccttcaa ctgttgctc 39

<210> 1384  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1384  
tgtaaaacga cggccagtgt ggtcttttaa ggaggcctg 39

<210> 1385  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1385  
tgtaaaacga cggccagtag atgtatggcg gaggtttct 39

<210> 1386  
<211> 39  
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